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Hoetten.G., Bechtold.R. and Pohl,J.
Monomeric protein of the tgf-g(b) family-
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Homo sapiens
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ETGLSTINOTRLDEHTSSDRTAGBREVQOASLMFFVOLESNTTWTLKVRULVLGPHNT

NLTLATOYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGOVAQSSVILLGGAAHR

PEYAARVRYGGKHOIHRRGIDCOGGSRNGCRQEFFVDFREIGWHDWIIOPECYAMNFC

IGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSXCVPTARRPLSLLYYDRDS

NLYKTDIPDMVVEAGGCS"

8 11 g 585 t 3 others
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          Mammalia; Eutheria; Pr
1 (bases 1 to 168473)
                                                                                                                                 Homo sapiens chromosome 12 clone RP11-772E1, WORKING SEQUENCE, 15 unordered pieces.
AC063917
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
                                                               Homo sapiens
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Muzny, D.M., Addams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Banbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Poster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Klaly, S., Khan, U., King, L., Korvah, J., Kover, C., Lewis, L., Li, J., Li, Li, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Li, J., Liu, M., Loulseged, H., Liu, J., Liu, K., Loulseged, H., Liu, J., Liu, M., Loulseged, H., Liu, J., Liu, M., Loulseged, H.,

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Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Pecry, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Pinus, E., Pu, L.L., Quiles, M., Ren, Y., Sodergren, E., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Walliams, G., Williams, A., Warren, R., Washington, C., Watlington, S., Wulliams, G., Williams, A., Mieczyk, R., Wooden, S., Worley, K., Wulliams, G., Williams, R., Zhou, J., Zorrilla, S., Nelson, D., Nelson, D., Weinstock, G. and Gibbs, R.
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On Jan 31, 2002 this sequence version replaced gi:11693210.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* CONSISTS of 15 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 25% of reads
Chemistry: Dye-terminator Big Dye: 75% of reads
Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hgschelp@bcm tmc.edu
Project Information
Center project name: HAUR
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Center code: BCM
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                                                         36529: contig of 36529 bp in length
36629: gap of unknown length
57746: contig of 21117 bp in length
57846: gap of unknown length
57846: gap of unknown length
77489: contig of 19643 bp in length
77599: gap of unknown length
91641: contig of 14052 bp in length
91741: gap of unknown length
100571: contig of 8830 bp in length
100571: gap of unknown length
112083: contig of 11412 bp in length
112083: gap of unknown length
112183: gap of unknown length
112183: gap of unknown length
112183: gap of unknown length
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112083:
112183:
120012:
120112:
120112:
129735:
gap of contig
unknown length
of 9623 bp in 1
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COMMENT

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Best Local Similarity 99.6%;
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                           34538 GCCAACACAGCTGCAGGCACCACTGGAGGGGGCTCATGCTGTACCCACGGCCCGGCGC
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                                                    1037 GCCAACACAGCTGCAGGCACCACTGGAGGGGGCTCATGCTGTGTACCCACGGCCCGGCGC 1096
1097 CCCCTGTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGACTGACATACCTGAC 1156
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                                          /db_xref="taxon:9606"
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154211: gap of u
157786: contig
157866: gap of u
16173: gap of u
161873: gap of u
165855: contig
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                               HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                     AC022506.32 GI:15809067
                                                                                     SEQUENCE, 7 unordered pieces.
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RES ALSDROOKS, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Barbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Barbrooks, S.L., Bartunge, H.C., Are, J.R., Bonuin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bouck, J., Bouck, J., Chor, R., Chocko, J., Chavez, D., Chen, G., Ch
Direct Submission

Direct Submission

Submitted (05-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 30, 2001 this sequence version replaced g1:14861641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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JOURNAL TITLE AUTHORS

REFERENCE

TITLE JOURNAL

COMMENT

Center: Baylor College of Medicine Center code: BCM

Contact: hgsc-help@bcm.tmc.edu Web site: http://www.hgsc.bcm.tmc.edu/

Center clone name: RP11-181L23 Center project name: HADT

Assembly program: Phrap; version 0.990329
Consensus quality: 184808 bases at least Q40
Consensus quality: 186378 bases at least Q20
Consensus quality: 18626 bases at least Q20
Consensus quality: 186079; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 7.7x in Q20 bases; sum-of-contigs estimation bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pleces

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BASE COUNT
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                                  ATAGCAGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCTCAATCTTCTCAAG
                                                   ATAGCAGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCTCAATCTTCTCAAG 1036
                                                                                                  TGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCAGTGCCCACTACAC
                                                                                                                                 TGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCAGTGCCCACTACAC
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/chromosome-"12"
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1. .181272
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78521: contig of 35443 bp in 1
78621: gap of unknown length
109061: contig of 30440 bp in 1
109161: gap of unknown length
139562: contig of 30401 bp in 1
139662: gap of unknown length
157019: contig of 17357 bp in 1
157019: gap of unknown length
170814: contig of 13695 bp in 1
170914: gap of unknown length
181272: contig of 10358 bp in 1
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99.5%;
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Pred. No. 0;
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                                   CCTTCATCCATTTTTTGTCCTTCTCTCTCTCTCTCTATGCCCTTAAGGGGTGACTTGCCT 1816
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RESULT 10 AC018805/c

LOCUS DEFINITION

Homo sapiens chromosome 12 clone RP11-564P5, WORKING SEQUENCE, 29 unordered pieces. AC018805 185688 bp NA HTG 07-JUL-2000

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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VERSION
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Center project name: H_NH0564P05

Sequencing vector: M13; 87%

Sequencing vector: Plasmid; 13%

Chemistry: Dye-primer ET; 87% of reads

Chemistry: Dye-terminator Big Dye; 13% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 175278 bases at least 040

Consensus quality: 176882 bases at least 030

Consensus quality: 176882 bases at least 030

Consensus quality: 176882 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 217000; agarose-fp
Insert size: 182888; sum-of-contigs
Quality coverage: 3.63 in Q20 bases; agarose-fp
Quality coverage: 4.26 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:6855245.
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Direct Submission
Submitted (03-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                                             'note="assembly_name:Contig21"
|5083. .17219
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10476. .12815
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Fang, J., Wang, S.-Q., Smiley, E. and
Direct Submission
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DLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLRGPRETLLEHQQRQEEYEIISF
ADTDLSSINQTRLEFHFSGRMASGMEVRQTRFMFFVFPHNATQTMNIRVLVLRPYDT
NLTLTSQYVVQVNASGWYQLLLGPEAQAACSGGHLTLELVPESQVAHSSLILGWFSHR
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/db_xref="taxon:10090"
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/protein_id="AAC53164.1"
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CTGAATATAGGCTTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTCCTTCC 147 ...
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structure, chromosomal localization, and expression analysis of the
mouse inhibin/activin beta C (Inhbc) gene
Genomics 32 (3), 358-366 (1996)
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Schmitt,J., Hotten,G., Jenkins,N.A., Gilbert,D.J., Copeland,N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-AUG-1995) H. Schrewe, Max-Planck-Institut Immunbiologie, Postfach 1169, D-79011 Freiburg, FRG
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/translation="MASSILLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLL
/translation="MASSILLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQREILLL
/translation="MASSILLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESYREYEYE
DLAKKSILDKLHLSQRPILGRPVSRCALKTALLQRLGPRATOTMNIRTLLCHPOETYT
ADTDLSSINGTRLEFHFSGRWASGMEVROTRFWFFVDFWATOTMNIRTLLCWFSVPT
NLTLTSQYVVQVNASGWYQLLLGPERQAACSQGHLTLELVPESQYAHSSLILGWFSHR
PFVAAQVRVEGKHRVRRRGIDCQGGSRWCCROEFFVDFREIGWNDWIIQPEGYAMNFC
TGQCPLHYAGGMPGISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDS
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Hoetten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
NOVEL GROWTH OR DIFFERENTIATION FACTOR OF THE TGF- beta FAMILY PATECHNIC (DE)
BIOPHARM GES ZUR BIOTECHNOLOGI (DE)
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Other publication DE 19511243 960104
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Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
DNA encoding growth/differentiation factor
Patent: US 5807713-A 3 15-SEP-1998;
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 TGTCTCTGCTCTATTATGACAGGGACAGCAGCATTGTCAAGACTGACATACCTGACATGG 1160
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                                                                    GTGACAGGGAGGTCCAGGCAGGCCAGTCTCATGTTCTTTGTGCAGCTCCCTTCCAATACCA 560
                                                                                                                           GCCTCTCCACCATCAACCAGACTCGTCGTCGATTTTTCACTTCTCCTCTGATAGAACTGCTG
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                                                      GTGGCATGGAGGTCCGGCAGACCCGCTTCATGTTCTTCGTGCAGTTCCCCCCACAATGCCA
                                                                                                            ACCTCTCCAGCATCAACCAGACCCGGCTCGAGTTCCACTT---CTCTGGTAGAATGGCCA 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified
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Pred. No. 6.1e-201;
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AAT19615

Claim 1; Page 10; 15pp; German. DNA encoding transforming growth factor beta MP-121 - has mitogenic for use in wound healing.

Ouery Match Best Local Similarity Matches 2271; Conserva CC a cDNA library prepared using total RNA from human liver was corrected to PCR amplification using primers corresp. to contain a new sequenced; one clone (clone) the tre-screen the human part of the signated products were corrected. The prosent sequence of the library from this clone was formating the prosent sequence) coding for a TGF beta like PCC comprising it or inducing properties making it of the protein was formatification that protein encoded by the cDNA library and also clone was comprising it or heterodimers of the protein was formatification useful for inducing tissue regeneration. Sequence 2272 BP; 510 A; 663 C; 513 G; 586 T; 0 other; Conservative 0; Mismatches

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121 CCCAGCAATGACCTCCTCATTGCTTCTGGCCTTTCTCCTCGCTCCTGGCTCCAACCACAGTGGC 180
121 CCCAGCAATGACCTCCTCATTGCTTCTGGCCTTCCTCGCTCCAACCACAGTGGC 180 rcccada a creace de reacta de la referencia de la referen

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1740 TACCTACCCCCCTCTTTGTTGTGAGCCCCCTGTCCTTAGTTGTCCAGGTGAACTACTA
1740 1621 CAGAGAGGCCCTTCTTTGGATTCACCAAAGTTTAGATCACTGCTGCCCAAAATAGAGGCT 1621 CAGAGAGGCCCTTCTTTGGATTCACCAAAGTTTAGATCACTGCTGCCCAAAATAGAGGCT 1680 CAGAGAGGCCCTTCTTTGGATTCACCAAAGTTTAGATCACTGCTGCCCAAAATAGAGGCT 1680 1561 CAATGGTCCCCACTCCAAGATGAGTTGACACACCCCTTCCCCCAATTTTTTGTGGATCTC 1620
1561 CAATGGTCCCCACTCCAAGATGAGTTGACACACCCCTTCCCCCCAATTTTTTGTGGATCTC 1620
1562 CAATGGTCCCCAACTCCAAGATGAGTTGACACAACCCCCTTCCCCCCAATTTTTTGTGGATCTC 1620 1501 CACCCTTAGCTCACCTTTAATAGACCCCATAACCCACTATGCCTTCCTGTCCTTTCTACT 1501 CACCCTTAGCTCACCTTTAATAGACCCCATAAACCCACTATGCCTTTCCTGTCCTTTCTACT 1560 DЪ 1441 CTCCAGGACTCAGACCCATCTCCAACCATGAGCAATGCCATCTGGTTCCCAGGCAAAGA 1500 1441 CTCCAGGGACTCAGACCCATCTCCAACCATGAGCAATGCCATCTGGTTCCCAGGCAAAGA 1500 1500 CTCCAGGGACTCAGACCCATCTCCAACCATGAGCAATGCCATCTGGTTCCCAGGCAAAGA 1500 1381 TGACCACTACCCTCTTTCCTAGGGCATAGTCCATCCGCTAGTCCATCCGCTAGTCCATCCCGCTAGCCCCA 1410 1381 TGACCACTACCCTCTTTCCTAGGGCATAGTCCATCCCGCTAGTCCATCCCGCTAGCCCCA 1440 1321 ATTACCCCACCTTTGACTTGAAGAAACCTTCATCTAAAGCAAGTCACTGTGCCATCTTCC 1380
1321 ATTACCCCACCTTTGACTTGAAGAAACCTTCATCTAAAGCAAGTCACTGTGCCATCTTCC 1380
1321 ATTACCCCACCTTTGACTTGAAGAAACCTTCATCTAAAGCAAGTCACTGTGCCATCTTCC 1380 1261 GGGAATGACCTCATTCTCTCTCCAGAATGTGGACTCCCTCTTCCTGAGCATCTTATGGAA 1320 ş 90 1201 GGGAGCCCAAGGTTGCATGGGAAAACACGCCCCTACAGAAGTGCACTTCCTTGAGAGGA 1260 1201 GGGCAGCCCAAGGTTGCATGGGAAAACACGCCCCTACAGAAGTGCACTTCCTTGAGAGGA 1260 1201 GGCAGCCCAAGGTTGCATGGGAAAACACGCCCCTACAGAAGTGCACTTCCTTGAGAGGA 1260 ЪЬ Ş В ş 1081 ACCCACGGCCCGGCGCCCCCTGTCTCTGCTGCTATTATGACAGGACAGCAACATTGTCAA 1140 1081 ACCCACGGCCCGGCGCCCCCTGTCTCTGCTCTATTATGACAGGACAGCAACATTGTCAA 1140 Дb 5 1021 GCTCAATCTTCTCAAGGCCAACACAGCTGCAGGCACCACTGCAGGGGGGGCTCATGCTGTGT 1080 8 Ş 8 Ş 901 GATTGGCTGGCACGACTGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGG 960 901 GATTGGCTGGCACGACTGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGG 960 901 GATTGGCTGGCACGACTGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGG 960 841 CGACTGCCAAGGAGGGTCCAGGATGTGCTGTTGGACAAGAGTTTTTTTGTGGACTTCCGTGA 900 781 GCCTTTTGTGGCAGCCCGGGTGAGAGTTGGGGGCAAACACCGAGATTCACCGACGAGGCAT 840
781 GCCTTTTGTGGCAGCCCGGGTGAGAGTTGGGGGCAAACACCCGAGATTCACCGACGAGGCAT 840 721 GCTGGTACTTGAAGGCCAGGTAGCCCAGAGCTCAGTCATCCTGGGTGGAGCTGATAG 780
721 GCTGGTACTTGAAGGCCAGGGTAGCCCAGAGCTCAGTCATCCTGGGTGGAGCTGCCCATAG 780 Page 2

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1921 GTGGCTATTCTGTGTCCCTACACTACCTGGCTACCCCCTTCCATGGCCCCAGCTCTGCCT 1980

1921 GTGGCTATTCTGTGTCCCTACACTACCTGGCTACCCCTTCCATGGCCCCAGCTCTGCCT 1980

1911 GTGGCTATTCTGTGTCCCTACACTACCTGGCTACCCCCTTCCATGGCCCCAGCTCTGCCT
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1981 ACATTCTGATTTTTTTTTTTTTTTTTGAAAGTTAAAAATTCCTTAATTTTTAT 2040
1981 ACATTCTGATTTTTTTTTTTTTTTTTGAAAGTTAAAAATTCCTTAATTTTTTAT 2040
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2041 TCCTGGTACCACTACCACAATTTACAGGGCAATATACCTGATGTAATGAAAAGAAAAAGA 2100
2041 TCCTGGTACCACTACCACAATTTACAGGGCAATATACCTGATGTAATGAAAAAGAAAAAGA 2100
                                                      2160 AAAAAGACAAAGCTACAACAGATAAAAAGACCTCAGGAATGTACATCTAATTGACACTACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF74421 standard; DNA; 2272 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF74421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                         Human; transforming growth factor-beta; monomeric protein; MP52; human; transforming growth factor-beta; wulnerary; antilucer; nootropic; MP121; dimeric protein; TGF-beta; vulnerary; gene therapy; bone; MP121; dimeric protein; TGF-beta; voteopathic; gene; ds. neuroprotective antiinfertility; connective tissue; ds. cartilage; dental; wound healing; connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TGF-beta Mp121 nucleotide sequence SEQ 1D NO:3.
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                EP1074620-A1.
                                                                                                                                                07-FEB-2001.
                                                                                                              06-AUG-1999;
                                                                              06-AUG-1999;
                                          (HYGE-) HYGENE AG C/O MAEDER & BAUMGARTNER TREUH.
            WPI: 2001-228100/24.
p-pspB;
          AAB70530
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
128..1186
                                                                                                                                                                                                                                           /*rag" a *MP121"
/product * transforming growth factor (TGF)-beta monomeric
/product * transforming growth factor (TGF)-beta monomeric
                                                                                                                                    99EP-0115613.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a protein (I) selected from the members of the transforming growth factor-beta (no f a cystein which is contentially which is contentially which is contentially the form the fermation of a cystein (I) nuclein a monomericle for dimer formation of a cystein (I) nuclein a cystein (I) encoding (I); (I) chapter of the transforming substitution of a cystein (I) nuclein a cystein (I) encoding (I); (I) cystein (I) host uttal compisition (V) contenting (II) capable of (II) encoding (I); (IV); (I) has will encode the prevention contenting (I); (IV) cystein (I) host uttal composition (V) contenting (II); and can be contentially contentially of contentially of contentially of cystein (II) or antihitis useful form of the sociated with bone cystein (II) or antihitis useful form of the sociated with bone cystein places of places and passed and individual of the sociated with connective tissue used indicated tilege damage or affecting bone growth is the connective tissue indicated tilege damage or individual song the cystein cystein which capable of tissue associated with connective tissue indicated tilege damage or inspance associated with connective tissue cystein tissue and a cardiance of the sociated with connective tissue that the cystein cystein tissue and a cardiance cystein tissue and a cardiance of the sociated with connective tissue of the cystein cystein tissue and a cardiance cardiance and/or cystein tissue and a cardiance cardiance and/or the mainteniance of induction of new utcers, burns of the sociation of the cystein cystein tissue and a cardiance cardiance of the cystein cystein
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181 CACTCCAGAGCTGGCGTCAGTGTCCAGCATGTGGGGGGCCCACCTTGGAACTGGAGAG 240
181 CACTCCCAGAGCTGGCGTCAGTGTCCAGCATGTGGGGGGCCCACCTTGGAACTGGAGAG 240
181 CACTCCCAGAGCTGGCGGTCAGTGTCCAGCATGTGGGGGCCCACCTTGGAACTGGAGAG 240
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301 CCAGCGCCAACACTGAACCGCCTGTGTCCAGAGCTGCTTTGAGGACTGCACTGCAGCA
301 CCAGCGCCAACACTGAACCGCCTGTGTCCAGAGCTGCTTTGAGGACTGCACTGCAGCA
301 CCAGCGCCCAACACTGAACCGCCTGTGTCCAGAGCTGCTTTGAGGACTGCACTGCAGCA
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361 CCTCCACGGGGTCCCACAGGGGCACTTCTAGAGGACAGGAACAGGAATGTGAAAT 420
161 CCTCCACGGGGTCCCACAGGGGCACTTCTAGAGGACAGGAACAGGAATGTGAAAT 420
161 CCTCCACGGGTCCCACAGGGGCACTTCTAGAGGACAACAGGGAACAGGAATGTGAAAAT 420
                                                                                                                480
421 CATCAGCTTTGCTGAGACAGGCCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTT 480
421 CATCAGCTTTGCTGAGACAGGCCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTT 480
421 CATCAGCTTTGCTGAGACAGGCCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTT 480
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pred. No. 0;
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	Oy 1081 ACCCACGGCCCCCCTGCCTCCTTCACACACACACACACAC	
	OY 841 CGATTGCGAGGGTCAAGGTTGGGGCAAACACCAGGTGCATCATCATCATCATCATAG 780 OY 841 CGACTGCCAAGGAGGTCAAGGTTGGGGGTGAACACCAGATTCAGCCATAG 780 Db 841 CGACTGCCAAGGAGGTCCAGGAGGTTGGGGGCAAACACCAGATTCACCGACGAGGAGATGCAAGACACCAGATTCACCAACACACATAC 780 Db 841 CGACTGCCAAGGAGGTCCAGGATGTGGGGCAAACACCACATTCACCACCAGAGGAT 840 OY 901 GATTGGCTGGCACGAGGTCCAGGAGGTCAAGAGAGTTTTTTTGTGGAACTTCCGTGA 900 Db 901 GATTGGCTGGCACGACTCAGGATTCATCTTCTTTTTTTTGTGACTTCCGTGA 900 OY 961 GCAGTGCCACTACCAGCATCAGCCTTCAGGCTTACGCACTTCCGTGA 900 OY 961 GCAGTGCCCACTACCAGGATCATCCAGCCTTAGGCCATGAACTTCTCTCGTGA 900 Db 961 GCAGTGCCCACTACCAGGCATCAGCCTTAGGCCATGAACTTCTCTCATAGG 960 OY 1021 GCTCAATACCAGGCATGCAAGGCTTACCTGCATTAGGCAACTTCTTCTAAACTTCTTCAAACACTTCTTCAAACACATACCAAGGAACATTCAACCATTCTTCAACACATTCTTCACACATTCTTC	
	, e 4 g 6 g 8 g 8	
u s	OY 481 CTCCTCTGATAGAACTGCTGGTGACACGC	

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KW KW KW AC
                                       sig_peptide
                                                           Liver activin; beta C; beta e; cell differentiation; haematopoiesis; bone; insular maturation; hormone; neuronal survival; menstrual disorder; transgenic; modulator; ss. is cythopoiesis; haemophilia; cystic fibrosis; immunoassay; immunoassay; immunoassay; immunoassay;
                                                                                                                         Murine liver activin beta c polypeptide encoding cDNA.
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                                                                                                                                                                                                                2221 GTTTTCCTGTTTTAAGCTGCAGTAACTTTTCTGACTATGGATCATCGTTCCTT 2272
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2161 TGCATTAATCAATAGCTGCACTTTTTGCAAACTGTGGCTATGACAGTCCTGAACAAGAAG 2220
220 TGCATTAATCAATAGCTGCACTTTTTGCAAACTGTGGCTATGACAGTCCTGAACAAGAAG 2220
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2101 AAAAGACAAAGCTACAACAGATAAAAGACCTCAGGAATGTACATCTAATTGACACTACAT 2160
2101 AAAAGACAAAGCTACAACAGATAAAAGACCTCAGGAATGTACATCTAATTGACACTACAT 2160
                                                                                                                                                                                                                                                                                                            2041 TCCTGGTACCACTACCACAATTTACAGGGCAATATACCTGATGTAATGAAAAGAAAAGA 2100
2041 TCCTGGTACCACTACCACAATTTACAGGGCAATATACCTGATGTAATGAAAAGAAAAAGA 2100
2061 TCCTGGTACCACTACCACAATTTACAGGGCAATATACCTGATGTAATGAAAAGAAAAAGA 2100
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1921 GTGGCTATTCTGTGTCCCTACACTACCTGGCTACCCCCCTTCCATGGCCCCAGCTCTGCCT 1980
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1681 TACCTACCCCCCTCTTGTTGTGAGCCCCTGTCCTTGTTAGTTGTCCAGGTGAACTACTA 1740
/*tag. a
/Product. "activin beta c Polypeptide"
149.208
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CC of haematopoiesis, erythroid differentiation, ovarian follicular canalysis, borneone secretion, neuronal survival, spermatogenesis, bone CC formation, insulin secretion or cardiac morphogenesis are some conditions CC that can be diagnosed using the liver activin. Cell growth and CC differentiation can be stimulated by treatment with an liver activin CC compound or agent that upregulates the compound's expression. Antagonists CC can be used to treat liver diseases while agonists can be used to treat liver diseases while agonists can be used to compound may also induce bone growth (e.g. for treating osteoporosis or compound may also induce bone growth (e.g. for treating osteoporosis or compound may also induce bone growth (e.g. for treating osteoporosis or compound may also induce bone growth (e.g. for treating osteoporosis or compound may also induce bone growth (e.g. for treating osteoporosis or contain hamunoassays, to generate anti-idiotypic antibodies (which compound to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, or modularors.
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Best Local 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding sub-units of liver activin useful for regulating growth and differentiation of cells, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating liver, bone and haematopoletic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1837 BP; 418 A; 531 C; 455 G; 433 T; 0 other;
                                                                                                                                                                                                                                                       105 CTGAATATAGGCTTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTCCTCCTTGC 164
165 TCCTGGCTCTTCTGTTCCTGACTCCAACCACAGTAGTGAACCCCAAAACTGAGGGTCCAT 224
                                                                                                                                                                                                              144 TTCTGGCCTTTCTCCTCCTGGCTCCAACCACAGTGGCCACTCCCAGAGCTGGCGGTCAGT 203
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                                                                                                                                                                                                                                                                                                   84 CTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC 143
                                                                                                                                                                                                                                                                                                                                            45 CACATTCCTCCCAGGGTCCCTGGTGCCCAGGACAGAGTTGAACCCACTCCCGTTGAGACC 104
                                                                                                                                                                                                                                                                                                                                                                 24 CACACTTCTTCCAGGGCCTCTGGCAGGCCAGGACAGAGTTGAGACCACAGCTGTTGAGACC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                           GTCCAGCATGTGGGGGGCCCACCTTGGAACTGGAGAGCCAGCGGGAGCTGCTTCTTGATC 263
                                                                                        GCCCAGCATGTTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGAGCTGCTTCTCGATT
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1460	AGGGCATAGTCCATCCCGCTAGTCCATCCCGCTAGCCCCACTCCAGGGACTCAGACCCAT	1401	Qγ
1384	AGGGATCCACCTCTAAAGAGAGTCACTAGTGACCAACAGCCTTTCTCTCTCTCTCTCTCTCTCTCTC	1331	Dь
1400	COTTCATCTAAAGCAAGTCACTGTGCCATCTTCCTGACCACTACCCTCTTTCC	w	Qy
1330	CTGTCCAGAATGGAAACACCTTTCTAAGCATGCAGACATCCCTCTGTGGACTTC	1277	рь
	TGTGGACTCCCTCTTCCTGAGCATCTTATC	1281	Qy
1276	GCCTTCCTCAGGAAGGGAAACTCTGTTCCCACTT	24	gg .
1280	GAAAACACGCCCCTACAGAAGTGCACTTCCTTGAGAGAGGAGGGAATGACCT0	1221	Оy
1241	TGGTCGAGGCCTGCGGGTGTAGTTAGCTTATGGGTGATACAGGCTGCCTGAGGTAGAATG	1182	В
1220	TAGAGGCCTGTGGGTGCAGTTAGTCTATGTGTGGTATGGGCAGCCCAAGGT	1161	у
1181		1122	망
1160	TCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGACTGACATACCTGACATG	1101	γo
1121		1062	dа
1100	CACAGCTGCAGGCACCACTGGAGGGGGGCTCATGCTGTGTACCCACGGCCCGCCGCCCCCC	1041	Qy
1061	ξ:	1002	рb
1040	AGGCATGCCTGGTATTGCCTGCCTCTTTCACACTGCAGTGCTCAATCTTCTCAAGGCCA	981	Oy
1001	CATCCAGCCTGAAGGCTATGCCATGAACTTCTGCACCGGGCAGTGCCCACTACATGTGG	942	Db
980	— თ		Qy
941	ACTTCCGTGAGATTGGCTGGAATGACTGGA	882	Db
920	CGACAAGAGTTTTTTGTGGACTTCCGTGAGATTGGCTGGC	861	νQ
881	AGGGGGCGTCCA	822	фd
860	GAGAGTTGGGGGCAAACACCAGATTCACCGACGAGGCATCGACTGCCAAGGAGGGTCCA	801	οy
821		762	В
900	AGCCCAGAGCTCAGTC	41	Qy
761	AAGCTCAAGCTGCTTGCAGCCAGGGACACCTTACTCTGGAGCTGGTACCAGAAAGCCAGG 7	702	ДĎ
740	AAGCTCAAGCTGCCTGCAGCCAGGGGGCACCTGACCCTGGAGCTGGTACTTGAAGGCCAGG 7	681	Qy
701	CAAGTCAGTACGTGGAGGTGAATGCCAGTGGCTGGTACCAGCTTCTCCTGGGACCTG	642	Db
60	TACT	621 (Оу
41	CCAGACCATGAATATAAGAGTTCTTGTGCTAAGACCATATGA	582 C	ф
20	TTGGAC	61	Qy
81	급=	522 G	Db
60	TGACAGGGAGGTCCAGCAGGCCAGTCTCATGTTCTTTTGTGCAGCTCCCTTCCAATACCA	01	Qy
21	CCTCTCCAGCATCAACCAGACCCGGCTCGAGTTCCACTTCTCTGGTAGAAT	465 A	Db
00	CCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTTCTCCTCTGATAGAACTGCTG 5	441 G	δ
64			gg ,
40	AGACAG 4	84	Oy
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83	AGGGGG 3	324 C	γQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1620 GTCACTGAAGATTATATTGCTGCCTTCCAAA 1650
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                                      8783..9533
/note= "activin beta e exon 2"
                                               /number- 1
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maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopolesis, particularly erythropolesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies (which
                                                        are useful in immunoassays, to generate anti-idiotypic antibodies (which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, containing the transgenic animals, are useful for screening for liver activin
                                                                                                                                                                                                                                                                                                                                                                                                                                derived from beta c cDNA clone is used for screening and cloning a liver activin beta e gene. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopolesis, erythroid differentiation, ovarian follicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopolesis, particularly erythropolesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This cDNA encodes a murine liver activin beta c polypeptide. Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders
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Matches

Local Similarity nes 883; Conserv

Conservative

0; Mismatches 306; Score 583.4; DE Pred. No. 2.1e-1

Indels

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   TTAATAGACCCCATAACCCACTATGCCTTCCTGTCCTTTCTACTCAATGGTCCCCACTCC 1576.
                                  CGACTGCCTACCACAAGGAATGTCATTTTGTT - CCTGGCAAACACACCCCTTAGCTCTCCC 3024
                                                               CCATCTCCAACCATGAGCAATGCCATCTGGTTCCCAGGCAAAGACACCCCTTAGCTCACCT 1516
                                                                                              TGCTGGGACATGGTTGACCC----AGTACACCCATCCTCAGCCTTAAGCTAGAGGCTAAT 2965
                                                                                                                             TCCTAGGGCATAGTCCATCCCGCTAGTCCATCCCGCTAGCCCCACTCCAGGGACTCAGAC 1456
                                                                                                                                                            CTTCAGGGGATCCACCTCTAAAGAGAGTCACT----AGTGCACAACAGCCTTTCTCTC '2909
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27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1637 TGGATTCACCAAAGTTTAGATCACTGCTGCCCAAA 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK52736;
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                                                                                                                                                                                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001;
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                                                                                                                                                                           activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT, Asundi Y, Zhao QA, Wang D, Wang J, Zhang J, Ren Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000;
                                                                                                                                          treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 4608; 6221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2000;
                                                      Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system disorder; arthritis; inflammation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM79603
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2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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                                                                  2111
from
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                                                                  (AAK52582) and 3666 the sequence listing
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         The sequences given in AAQ47709-10 represent embryo and liver derived human transforming growth factor-beta (TGF-beta) genes repectively. The proteins encoded by these sequences may be used in a pharmaceutical composition for the treatment of various bone, cartilage or tooth
                                                                                                                       New transforming growth factor-beta family proteins and DNA used in tissue and wound repair, in treatment of bone, cartilage
 defect's and in tissue and wound repair processes.
                                                                                    Claim 4; Page 18; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transforming growth factor; beta; TGF-beta; pharmaceutical; bone; cartilage; tooth; wound repair; immunosuppressor; organ transplant; cosmetic surgery; antibody; diagnosis; ss.
                                                                                                                                                                        P-PSDB; AAR45447
                                                                                                                                                                                                               Hoetten G,
                                                                                                                                                                                                                                       (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                               12-FEB-1993;
                                                                                                                                                                                                                                                                                                                           19-AUG-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ47710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1606 BP; 465 A; 231 C; 491 G; 419 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                             defects, and antibodies for diagnosis
                                                                                                                                                                                                               Neidhardt H;
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2..265
/*tag= a
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These proteins
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                        Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                  01-SEP-2000;
15-SEP-2000;
                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                        05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK51752 standard; cDNA; 1783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cosmetic surgery. Antibodies used for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may also be used as immunosuppressors in organ transplants and in cosmetic surgery. Antibodies raised against these proteins may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 CACAGCTGCAGGCACCACTGGAGGGGGCTCATGCTGTGTACCCACGGCCCCGGCGCCCCCT 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AGTAGAGGCCTGTGGGTGCAGTTAG 265
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                                                                     Liu C,
Wang D,
                                                            Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                      2000US-0496914
2000US-0560875
2000US-0598075
2000US-0620325
2000US-0623325
2000US-0654936
2000US-0663325
2000US-0728422
                                                                     Drmanac RT, Asundi V, Zhou
, Wang J, Zhang J, Ren F, (
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Pred. No. 1.9e-52;
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Nucleic acids encoding polypeptides with cytokine-like activities

P-PSDB; AAM78619

WPI; 2001-476283/51.

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80392) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhable activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1259-1260; 6221pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1602 TATTGAAAAGTTAAAAATTCCTTAATTTTTTATTCCTGGTACCACTACCACAATTTACAG 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1783 BP; S11 A; 265 C; S19 G; 488 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 4431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intlammation.
21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                 chemokinetic; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                   AAI60442 standard;
                                               26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                leukaemia; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTGACTATGGATCATCGTTCCTT 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTGACTATGGATCATCGTTCCTT 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTCAGGAATGTACATCTAATTGACACTACATTGCATTAATCAATAGCTGCACTTTTTG 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                   (first entry)
2000US-0488725
2000US-0552317
                                                                                                                                                                                                                                                                                                                                                                                                     CDNA; 3678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                 drug
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                                                                                                                                                                                                   screening;
                                                                                                                                                                                                   arthritis; inflammation;
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AAT19615/c ID AAT19615 standard;

CDNA

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28-JUN-1996

(first entry)

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                                                                                                                                                                                                                                                                                                                     Matches 264;
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          in gene therapy. A composition containing a polymphic or polympuleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitites such as: Immune system suppression, Activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                 C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4431; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                 specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-442253/47.
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1326
                                                             1386
                                                                                                                          1446
                                                                                                                                                                                                                                                      1566
                                                                                                                                                                                                                                                                       2008 TTTTGAAAAGTTAAAAATTCCTTAATTTTTTATTCCTGGTACCACTACCACAATTTTACAG 2067
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3678 BP; 1117 A; 550 C; 877 G; 1134 T; 0 other;
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                                                                               CAAACTGTGGCTATGACAGTCCTGAACAAGAAGGGTTTCCTGTTTAAGCTGCAGTAACTT 2247
                TTCTGACTATGGATCATCGTTCCTT 2272
                                                             CAAACTGTGGCTATGACAGTCCTGAACAAGAAGGGTTTCCTGTTTAAGCTGCAGTAACTT
                                                                                                                          ACCTCAGGAATGTACATCTAATTGACACTACATTGCATTAATCAATAGCTGCACTTTTTG
                                                                                                                                                                                                                    GGCAATATACCTGATGTAATGAAAAGAAAAAGAAAAAGACAAAGCTACAACAGATAAAAG 2127
                                                                                                                                                                                                                                                        TATTGAAAAGTTAAAAATTCCTTAATTTTTTATTCCTGGTACCACTACCACAATTTACAG 1507
TTCTGACTATGGATCATCGTTCCTT 1302
                                                                                                                                                                                         GGCAATATACCTGATGTAATGAAAAGAAAAAGAAAAAGACAAAGCTACAACAGATAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
; 2000US-0693036.
; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                    Conservative
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Wehrman T,
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99.6%;
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, Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Score 263.4;
                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.2e-51;
                                                                                                                                                                                                                                                                                                                                                      DB 22;
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                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                    Length 3678;
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Human gene signature HUMGS00682

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                                                                                                                                                                                                                                                                                                                                                                                                      Matches 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of. human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA as initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a CDNA library can be determined 'con meion retimers and orehood from the GS.
                                                                                                                                                                                                             2069 GCAATATACCTGATGTAATGAAAAGAAAAAGAAAAGACAAAGCTACAACAGATAAAAGA 2128
                            2249 TCTGACTATGGATC 2262
                                                                                                                                                                                                                                                         Sequence 254 BP; 74 A; 41 C; 46 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 432; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                     194
                                                                                                                                                                                                                                                                                                                                                                                                                                   recognising different cell types.
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TCTGACTATGGATC 1
                                                                                                                          CCTCAGGAATGTACATCTAATTGACACTACATTGCATTAATCAATAGCTGCACTTTTTGC
                                                                                                                                             CCTCAGGAATGTACATCTAATTGACACCTACATTGCATTAATCAATAGCTGCACTTTTTGC
                                                           AAACTGTGGCTATGACAGTCCTGAACAAGAAGGGTTTCCTGTTTTAAGCTGCAGTAACTTT
                                                                                                                                                                                              GCAATATACCTGATGTAATGAAAAGAAAAAAGAAAAAGACAAAGCTACAACAGATAAAAGA 135
                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                11.2%;
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                             Score 254; DB 16;
Pred. No. 6.9e-50;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 254;
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RESULT 10
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                                                                                                                                                                                                                                                                                                P-PSDB; AAB36521.
                                                                                                                                                                                                                                                                                                          WPI; 2000-619230/59.
                                                                                                                                                                                                                                                                                                                               Lu PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC87968 standard; cDNA; 5214 BP
                                                                                                                                                                                                                                                                                                                                                 (ARBO-) ARBOR VITA CORP
                                                                                                                                                                                                                                                                                                                                                                                                    21-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse CLASP-1 nucleotide sequence SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                    2000US-0176195.
2000US-0182296.
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                                                                                                                                                                                                                                                                                                                                                                                       99US-0134114.

99US-0134117.

99US-0134118.

99US-0160860.

99US-0162498.

99US-0170453.
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inflammatory responses -Isolated cadherin-like asymmetry protein-2 polynucleotide and polypeptide used to diagnose, treat and prevent autoimmune diseases and

Claim 1; Page 271-276; 286pp; English.

CC (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiarthritic, cytostatic, hypotensive, antirheumatic, CC antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, CC antianaemic, haemostatic and neuroprotective activities (CLASP-2 can be CC used to inhibit an immune response in a subject by interfering with the CC ability of a CLASP-2 protein to bind to another T cell or B cell. An CC immune response in a subject may also be inhibited by administering an commune response in a subject may also be inhibited by administering an cC immune response in a subject may also be inhibited by administering an cC proteins and antibodies can be used to prevent or treat a CLASP-2 cC mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat the prevent immune responses and cC augment immune responsiveness in immunodeficiency states, inhibit cc proliferation and differentiation of cells involved in an inflammatory can exacerbated in an inflammatory considered and increase and increase c.g. arthritis, inflammatory bowel disease and increase consense e.g., arthritis, inflammatory consense e.g., arthritis, inflammatory consense e.g., arthri treated by disrupting CLASP-2 function include multiple sclerosis, rheumatoid arthritis, endometriosis and pregnancy induced hypertension The present sequence encodes mouse CLASP-1 which is used in the of the present invention

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2074 ATACCTGATGTAATGAAAAGAAAAAGAAAAAGACAAAGCTACAACAGATAAAAGACCTCA 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2194
The present sequence encodes a cadherin-like asymmetry protein to designated Clasp-1. The Clasp-1 protein is a cell surface protein which contains certain classical cadherin characteristics, but exhibits an apical distribution pattern on the surface of lymphocytes. The membrane location of the protein correlates with the contact interface between T and B cells, and antibodies against an extracellular domain of the CLASP-1 protein disrupt T cell/B cell interactions. The Clasp-1 protein thus inhibits immune response. The polypeptide is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cadherin-11ke asymmetry protein-1; Clasp-1; immune response; autoimmune disease; hypersensitivity; transplantation rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding a murine cadherin-like asymmetry protein-l (Clasp-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200020434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunodeficiency; lymphocyte marker; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
                                                                                                                                                                                                                                                                                                                                             02-OCT-1998;
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                                                                                                                                           Claim 3; Page 69-74; 86pp; English.
                                                                                                                                                                                       New isolated polynucleotides and polypeptides encoding mammalian . CLASP-1 protein, useful for inhibiting an immune response, especially.
                                                                                                                                                                                                                                    P-PSDB; AAY84808.
                                                                                                                                                                                                                                                                                 Lu PS,
                                                                                                                                                                                                                                                                                                             (STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                        treating autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGCTATGACAGTCCTGAACAAGAAGGGTTTCCTGTTTAAGCTGCAGTAACTTTTCTGA 2253
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                                                                                                                                                                                                                                                                                   Davis MM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "cadherin-like asymmetry protein-1 (Clasp-1)"
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Pred. No. 2.2e-35;
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AAS75540/c
ID AAS755
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibiting an immune response, especially in treating an autoimmune disease and hypersensitivities, prevention of transplantation rejection responses and augmentation of immune responsiveness in immunodeficiency states. The protein may also be useful for identification of the therapeutic molecules that function by inhibiting or stimulating the biological activity of Clasp-1. The Clasp-1 polynucleotide may be used for diagnostic and therapeutic purposes, especially for detecting the expression of Clasp-1 as a lymphocyte marker and may be used to detect Clasp-1 gene expression of aberrant Clasp-1 gene expression in disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5214 BP; 1581 A; 1133 C; 1130 G; 1370 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          states e.g. gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2074 ATACCTGATGTAATGAAAAGAAAAAGAAAAGACAAAGCTACAACAGATAAAAGACCTCA 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS75540 standard; cDNA; 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2134 GGAATGTACATCTAATTGACACTACATTGCATTAATCAATAGCTGCACTTTTTGCAAACT 2193
                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #11344.
                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS75540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2254 CTATGGATCATCGTTCCTT 2272
                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 CTATGGATCATCGTTCCTT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 ACATGTGATGTAATGAAAAGAAAAAGAAAAGACAAAGCTACAACAGATAAAAGACCTCA 271
                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                     31-MAR-2000;
                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                               food supplement;
 biodiversity
                                                                                                                                                                                          23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAATGTACATCTAATTGACACTACATTGCATTAATCAATAGCTGCACTTTTTTGCAAACT 211
                                                                                              2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                             ABG11353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                          2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.5%;
                                                                                                                             Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 194.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5214;
                                                                                                                                                                                                                                                                                                                                                                                      forensic;
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The invention relates to isolated polynucleotide (I) and

Claim 1; SEQ ID No 11344; 103pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC polymertide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II), (I) and (II) are useful in medical imaging of sites expressing (II), (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, Identification of mutations in CC esponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AASG4197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC at fire wiso intrombination or this patent did not appear in the printed constituents on the printed of account of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                 03-APR-1998;
28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
(CHIR ) CHIRON CORP
                                                                                                                                                                           05-AUG-1999
                                                                                                                                                                                                                                                                                     Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer;
                                                                                                                                                                                                                                                                                                                                        Human gene expression product cDNA sequence SEQ ID NO:5047.
                                                                                                                                                                                                            W09938972-A2
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ17574 standard; cDNA; 825
                                                                                                                                         20-JAN-1999;
                                                                                                                                                                                                                                                                                genetic
                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ17574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2188 C-AAACTGTGGCTATGACAGTCCTGAACAAGAAG 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2129 CCTCAGGAATGTACATCTAATTGACACTACATTGC-ATTAATCAATAGCTGCACTTTTTG 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2069 GCAATATACCTGATGTAATGAAAAGAAAAAGAAAAAGACAAAGCTACAACAGATAAAAAGA 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 899 BP; 239 A; 116 C; 285 G; 259 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   719 CAAAACTGTGGCTATGACAAGTCCTGAAACAAAG 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCAGGAATGTACATCTAATTGACACTACATTGCAATTAACAAATAGCTGCACTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAATATACCTGATGTAATGAAAAGAAAAAGAAAAAGACAAAGCTACAACAGATAAAAGA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201; Conservative
                                                                                                                                                                                                                                                                     analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 93.9%;
                                                                                    98US-0080666
98US-0072910
                                                 98US-0075954.
98US-0080114.
                                 98US-0080515
                                                                                                                                        99WO-US01619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 172.4;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4e-30;
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PA (HYSE-) HYSEQ INC.

XX

PI Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;

PI Scobedo J, Garcia PD, Garcia V, Giese K, Innis MA;

PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;

PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;

PT Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;

PT Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;

XX

PT Novel human genes and their expression products which are differentially expressed in different cell types

XX

Novel human genes and their expression products which are differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising the sequences given in AAX12532 to AAX17779. Also described is cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product is acteating at least one cancerous, where the gene product is encoded by one comprising detecting at least one suspected of being cancerous, where the gene product is encoded by one compine the sed polymucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, can be used for raising antibodies for experimental, diagnostic and detection of polymorphisms. Polypoptides may also be used to vocalls (e.g. to identify abnormal or diseased utssue in a human, to cancerous, the polymorleotides may also be used to off an two cells (e.g. to identify abnormal or diseased tissue in a human, to cancerous, the polymorleotides of the invention are especially used in the CC diagnosts, prognosis and management of colorectal cancer, breast cancer, ce peptide analogues and antagonists.

Sequence 825 BP; 239 A; 120 C; 162 G; 252 T; 52 other:
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Sequence 825 BP; 239 A; 120 C; 162 G; 252 T; 52 other;

Query Match
6.8%; Score 153.8; DB 20; Length 825;
Best Local Similarity 90.6%; Pred. No. 3.2e-26;
Matches 231; Conservative 0; Mismatches 14; Indels 10; Gaps

E Murine liver activin beta e polypeptide encoding cDNA.

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                                                                                                                                                                                                                                                              CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone confirmation, insulin secretion or cardiac morphogenesis are some conditions contact can be diagnosed using the liver activin. Cell growth and confirmation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to compound may also induce bone growth (e.g. for treating osteoporosis or costeomalacia) or haematopoiesis, particularly erythropolesis, e.g. for creating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which to liver activin receptors) and to inhibit liver activin. Also, containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, containing and containing for liver activin modified forms) proteins, containing the useful for screening for liver activin
                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liver activin; beta c; beta e; cell differentiation; haematopolesis; erythroid; ovarian follicular maturation; hormone; neuronal survival spermatogenesis; bone; insulin; cardiae morphogenesis; osteoporosis; osteomalacia; erythropolesis; haemophilia; cystic fibrosis; immunoas; menstrual disorder; transgenic; modulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA encodes a murine liver activin beta e polypeptide. Sequences derived from a beta c cDNA clone is used for screening and cloning the activin beta e gene. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopoiesis, erythroid differentiation, ovarian follicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9822492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 2; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW60618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1998.
                                                                                                                                                                                                           Sequence 2125 BP; 481 A; 573 C; 575 G; 496 T; 0 other;
                                            932
                                                                 904 TGGCTGGCACGACTGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCA 963
                                                                                                                        Local Similarity es 232; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-312408/27.
                                            CTGTGAGCCTGAGACCCCCTTATGTTGTAGGCGAGACCACTATGTAGACTTCCAGGAGCT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fang J;
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0752919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US20882
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216..278
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216..1268
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279..1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
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                                                                                                                                           6.78;
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                                                                                                                            0;
                                                                                                                                             Score 153; DB 1
Pred. No. 7e-26;
                                                                                                                            Mismatches
                                                                                                                                                                   DB 19; Length 2125;
                                                                                                                               105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1144 TGACATACCTGACATGGTAGTAGAGGCCTGTGGGTGCAGTTAG 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084
                                     A Xenopus laevis liver-derived DNA library in Charon 28 vector, was screened with a rat activin beta-A cDNA probe. Five clones were isolated, including clone M3. They were subcloned in pUC19 and used to transform competent E.coli HB101 cells. Transformant E.coli HB101/PXar3 coding for the M3 BMP was sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encodes Xenopus Bone Morphogenetic Factor M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ10891 standard; DNA; 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1024 CAATCTTCTCAAGGCCAACACAGCTGCAGGCACCACTGGAGGGGGGCTCATGCTGTACC 1083
                                                                                                                       Claim 5; Fig 2; 28pp; English.
                                                                                                                                                                Xenopus laevis bone morphogenetic protein and DNA encoding
                                                                                                                                                                                                        WPI; 1991-075112/11.
                                                                                                                                                                                                                                                                                                       20-JUL-1990;
06-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                     EP416578-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis
Sequence
                                                                                                                                                  used in
                                                                                                                                                                                           P-PSDB; AAR10991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           964 GTGCCCACTACACATAGCAGGCATGCCTGGTATTGCTGCTCCTTTCACACTGCAGTGCT 1023
                                                                                                                                                                                                                                                                (SCIT-) SCITECH RESEARCH CO.
                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEMICAL IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  992 GGGGTGGCGGGATTGGATCCTGCAGCCGGAGGGATACCAGCTGAATTACTGCAGTGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis; fracture; cartilage; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGGCCCGGCGCCCCTGTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGCCTCCTCAAAGCCAACAACCCT----TGGCCTGCGGGTTCTTCCTGCTGTGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCCCGCCCCACCTGGCAGTCCTGGCATTGCTGCCTCCTTCCATTCTGCCGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTGCACGAAGGCCTCTCTCTCTCTCTACCTTGACCATAATGGCAATGTGGTCAAGAC
                                                                                                                                                  therapy of fracture or osteoporosis
 687 BP;
                           AAQ10890 and AAQ10892-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                   Ueno N,
                                                                                                                                                                                                                                                                                                        90JP-0190774.
89JP-0229250.
                                                                                                                                                                                                                                                                                                                                                  90EP-0117079
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 2..478
 210 A; 145 C; 149 G; 179 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag*
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Search completed: October 11, 2002, 22:14:29 Job time: 332.267 secs

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ALIGNMENTS

RESULT 1 US-08-482-577B-1 (S-904-682-577B-1) Sequence 1, Application US/08482577B Patent No. 5807713 Patent No. 1NFORMATION: US-08-482-577B-1 TELEFAX: 202/638-4810 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2272 base pairs APPLICANT: APPLICANT: APPLICANT: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: NAME: KLESNER, SHARON REGISTRATION NUMBER: 36, CORRESPONDENCE ADDRESS: TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS NUMBER OF SEQUENCES: 49 REFERENCE/DOCKET NUMBER: P5 TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000 TOPOLOGY: linear MOLECULE TYPE: DNA ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM STREET: 655 FIFTEINTH STREET, N.W., G STREET LOBBY STREET: SUITE 330 FILING DATE: CLASSIFICATION: 435 COUNTRY: STATE: CITY: STRANDEDNESS: TYPE: nucleic acid APPLICATION NUMBER: TELEPHONE: 20005 WASHINGTON g USA BECHTOLD, ROLF HOTTEN, GERTRUD single JENS US/08/482,577B 36,335 P564-5010 N.W., G STREET LOBBY

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Best Local Similarity Matches 2272; Conserv

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FILING DATE: 12-AUG-1994
PRIOR APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: POT/EP93/00350
FILING DATE: 12-FEB-1993
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 9564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                           Matches 2272;
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TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA from mRNA
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BECHTOLD, ROLF
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Qy	7	GCAAACACCAGATTCACCGACGAGGCAT 8	
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Qy	84	GACAAGAGTTTTTTGTGGACTTCCGTGA	8
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Qy	901 GATTGGCTGGCACGACTGGATCATCCAGCCT		
Db	901 GATTGGCTGGCACGACTGGATCATCCAC	GGCTACGCCATGAACTTCTGCATAGG 9	
γQ	9	ATTGCTGCCTCCTTTCACACTGCAGT 1	N
Дb	961 GCAGTGCCCACTACACATAGCAGGCATO	ATTGCTGCCTCCTTTCACACTGCAGT 1	
Ωγ	1021 GCTCAATCTTCTCAAGGCCAACACAGCTGC	:AGGCACCACTGGAGGGGGGCTCATGCTGTGT 1	Ó
Дb	1021 GCTCAATCTTCTCAAGGCCAACACAGCTGC	ACCACTGGAGGGGGCTCATGCTGT	- œ
Qy	1081 ACCCACGCCCGGCGCCCCCTGTCTCTGCTC	TATTATGACAGGGACAGCAACATTGTCAA	يا ح
Db	1081 Acccaceecceecceccererere	TATTATGACAGGGACAGCAACATTGTC	í
οy	1141 GACTGACATACCTGACATGGTAGTAGAGGC	CTGTGGGTGCAGTTAGTCTATGTGTGTAT 1	20
3	1141 GACTGACATACCTGACATGGTAGTAGAGGC	GTGGGTGCAGTTAGTCTATGTGTGGT	1200

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GGTTTCCTGTTTAAGCTGCAGTAACTTTTCTGACTATGGATCATCGTTCCTT 2272
              GGTTTCCTGTTTAAGCTGCAGTAACTTTTCTGACTATGGATGATCGTTCCTT 2272
                                                    AAAAGACAAAGCTACAACAGATAAAAGACCTCAGGAATGTACATCTAATTGACACTACAT 2160
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; Patent No. 6171584
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Query Match 100.0%; Score 2272; Best Local Similarity 100.0%; Pred. No. 0, Matches 2272; Conservative 0; Mismatches
                                                                                                                                                                                          TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195
EFILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, Monica Chin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679
APPLICATION NUMBER: 12-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP
FILING DATE: 2-FEB-1993
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APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
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APPLICATION NUMBER: EP 9:
FILING DATE: 12-FEB-1992
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APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
STREET: Suite 330

CITY: Washington
STATE: DC
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APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: USE GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TELEPHONE: 202/638-4810
                                                                                                                         TOPOLOGY:
                                                                                                                                        TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,105
                                                                                                                                                                              LENGTH:
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ZIP: 200
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OPERATING SYSTEM: PC-DOS/MS-DOS
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BECHTOLD, Rolf
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	A 1140	1081 ACCCACGGCCCGGCGCCCCTGTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAA	Qγ
	T 1080	CTCAATCTTCTCAAGGCCAACACAGCTGCAGGCACCACTGGAGGGGGGCTCATGCTGTG	망
	108	1 GCTCAATCTTCTCAAGGCCAACACAGCTGCAGGCACCACTGGAGGGGGCCTCATGCTGTG	οy
	T 1020	61 GEAGTGCCCACTACACATAGCAGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAG	В
	T 1020	CAGTGCCCACTACACATAGCAGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAG	Q
	G 960	901 GATTGGCTGGCACTGGATCATCCAGCCTGAGGCTACGCCATGAACTTCTGCATAGC 	D 0y
	2	41 CGACTGCCAAGGAGGGTCCAGGATGTGCTGTCGACAAGAGTTTTTTTGGACTTCCGTG	Db
	900	. 4	9
	I 840	CCTTTTGTGGCAGCCCGGGTGAGAGTTGGGGGCAAACACCAGATTCACCGACGAGGG	dd
• •	840	781 GCCTTTTGTGGCAGCCCGGGTGAGAGTTGGGGGCAAACACCAGATTCACCGACGAGGCAT	Qy
	78	721 GCTGGTACTTGAAGGCCAGGTAGCCCAGAGCTCAGTCATCCTGGGTGGAGCTGCCCATAG	Db Oy
	72	AACTCCCCCTAGGGCCTGAAGCTCAAGCTGCCTGCAGCCAGGGGCACCTGACCCTGG	рb
	72	661 TCAACTCCCCCTAGGGCCTGAAGCTCAAGCTGCCTGCAGCCAGGGGGCACCTGACCCTGA	Qy
	6	GCTGGC	Db
	660	NACCTCACCTTGGCTACTCAGTACCTGCTGGAGGTGGATGCCAGT	οy
	600	541 GCAGCTCCCTTCCAATACCACTTGGACCTTGAAAGTGAGAGTCCTTGTGCTGGGTCCACA	밁
	600	CAGCTCCCTTCCAATACCACTTGGACCTTGAAAGTGAGAGTCCTTGTGCTG	οy
	540	481 CTCCTCTGATAGAACTGCTGGTGACAGGGAGGTCCAGCAGGCAG	P 6
	480		Db
	480	ATCAGCTTTGCTGAGACAGGCCTCTCCACCATCAACCAGACTCGTCTTGATTTTC	δ
	420	361 CCTCCACGGGTCCCACAGGGGCACTTCTACAGGACACAGGGACACAGGAATGTGAAAT	pb Qy
	s d	O1 CCAGCGCCCAACACTGAACCCGCCCTGTGTCCAGAGCTGCTTTGAGGACGAACACTGCAAA	₽
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	0	241 CCAGCGGGAGCTGCTTCTTGATCTGGCCAAGAGAAGCATCTTGGACAAGCTGCACCTCAC	B 5
		81 CACTCCCAGAGCTGGCGGTCAGTGTCCCCCAACATGTGGGGGGCCCCACCTTGGAACTGGAC	рb
مد	4.	181 CACTOCCAGAGCTGGCGGTCAGTCTCCAGCATGTGGGGGGGCCCCACCTTGGAACTGGAGAG	Qy
	180	121 CCCAGCAATGACCTCCTCATTGCTTCTGCCCTTTTCTCCTCCTGGCTCCAACCACACACA	D Qy
	0 N	61 TTGAGACCACAGCTGTTGAGACCCTGAGCCCTGAGTCTGTATTGCTCAAGAAGGCCCTGAGTCTGAGACGCCACAGAAGGACCCCTGAGTCTGAGACGACAGAAGGACCCTGAGAGAAGGACCACACAGAAGAAGGACCACACAGAAGAAG	Вb
	20	1 TTGAGACCACAGGTGTTGAGACCCTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCCTTC	Qy
•	60	1 CANGGAGCCATGCCAGCTGGACACACACTTCTTCCAGGGCCTCTGGCAGCCAGGACAGAG	B &
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                                                                                                                           Query Match
Best Local Similarity
                                                                                                                   Matches 2272;
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INFORMATION FOR SEQ ID NO:
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APPLICANT: H TTEN, GERTRUD
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                                                                                                                                                                                    TOPOLOGY: 110 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: EPO 9
FILING DATE: 12-FFB-100-
PRIOR ADDITE: 12-FFB-100-
PRIOR ADDITE: 12-FFB-100-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/289,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY, STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
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APPLICANT:
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                     61 TTGAGACCACAGCIGTTGAGACCCTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCCTTC 120
                                                                                                                                                                                                                                                                                                                             NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
                                                                                                                                                                                                                                                                                                                                                              NAME:
                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                    TYPE
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                                                   nucleic acid
EDNESS: both
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BECHTOLD, ROLF
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                                                                                                                                                                                    CDNA from mRNA
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12-FEB-1993
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100.0%; Pred. No. 0;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
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NAME: KLESNER, SHARON
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
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BECHTOLD, ROLF
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Pred. No. 5.1e-189;
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US-09-218-176-3
                                                                                        Sequence 3, Application US/09218176 Patent No. 6171584
                                                                 GENERAL INFORMATION:
                         APPLICANT:
    APPLICANT:
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NEIDHARDT, Helge
BECHTOLD, Rolf
                                         H TTEN, Gertrud
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US-09-218-176-3
                                                                                                                                                                                                     Matches 959;
                                                                                                                                                                                                                   Query Match 34.4%; Score 781; DB 4; I
Best Local Similarity 79.9%; Pred. No. 5.1e-189;
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202/638-4810 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA Chin
REGISTRATION NUMBER: 36,10
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 9: FILING DATE: 12-FEB-1992 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-JUL-1
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PRIOR APPLICATION NIMBER: 08/679,048
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
144 TTCTGGCCTTTCTCCTCGTGGCTCCAACCACAGTGGCCACTCCCAGAGCTGGCGGTCAGT 203
                                             87
                                                             84 CTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC 143
                                                                                                                                                     24 CACACTTCTTCCAGGGCCTCTGGCAGCCAGGACAGAGTTGAGACCACAGCTGTTGAGACC 83
                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202/638-4810
                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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FILING DATE: 01-JUL-1994
                                                                                                                 28 CACATTCCTCCCAGGGTCCCTGGTGCCCAGGACAGAGTTGA-AGCACTCCCGTTGAGACC 86
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: NIKAIDO, MARWELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth Street, N. W., G Street Lobby. STREET: Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                     CTGAATATAGGCTTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTCCTTGC 146
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1221 G 1221
                                              1164 TGGTCGAGGCCTGCGGGTGTAGTTAGCTTATGGGTGATACAGGCTGCCTGAGGTAGAATG
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                                                                                                                                        TGTCTTTGCTCTACTATGACAGGGACAGCAGCATTGTCAAGACGGATATACCTGACATGG
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                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                   Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                     TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GROWTH,
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NEIDHARDT, HELGE APPLICANT: BECHTOLD, ROLF APPLICANT: POHL, JENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE P 44 23 190.3 FILING DATE: 07-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY, STREET: SUITE 330 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                               APPLICATION NUMBER: US 08/289,222 FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: EPO 92102324.8 FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 25-AUG-1999
                                  982 AGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCTCAATCTTCTCAAGGCCAA 1041
                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202/638-4810
TETEFAX: 202/638-4810
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                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                       TYPE:
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   61
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20005-5701
                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                         202/638-5000
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                                                                                                                                                                                                                       cDNA from mRNA
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                                                                                                                                                    11.7%; Score 265; DB 3; 100.0%; Pred. No. 2.7e-58;
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US-09-054-526B-5
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                                                                             Query Match
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Patent No.
                                               Matches
                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                   TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
                                                                                                                                  MOLECULE TYPE:
922 CATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCAGTGCCCACTACACATAGC 981
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/054,526B FILING DATE: 03-APR-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1102 GTCTCTGCTCTATTATGACAGGGACAGCAAGATTGTCAAGACTGACATACCTGACATGGT 1161
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Dolo-
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                                      Match 100.0%; P
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                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                                                                                        NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/EP93/00350 FILING DATE: 12-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 12-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON
STATE: DC
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BECHTOLD, ROLF
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                                                                                                                                cDNA from mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1992
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                                                     11.7%; Score 265; DB 4; 100.0%; Pred. No. 2.7e-58;
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                                          Mismatches
                                                                        DB 4; Length 265;
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US-08-455-550-2
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                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056
FILING DATE: 30 APR-1993
APPLICATION NUMBER: 07/577
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: EFFORMET OF SEPENSION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                           HYPOTHETICAL: I
                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
            ORIGINAL SOURCE:
                            FRAGMENT TYPE
                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
                                                                                                                                                                            TELEFAX: 61,
TELEFAX: 200291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MURAKAMI, KAZUO APPLICANT: UENO, NAOTO APPLICANT: KATO, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1102 GTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGACTGACATACCTGACATGGT 116
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                                                                                                                                                                                    TELEPHONE: 617-523-6440
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                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 3:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08274215A Patent No. 5831054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
TELEFAX: 619-68-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1129 CAACATTGTCAAGACTGACATACCTGACATGGTAGTAGAGGCCTGTGGGTGCAGTTAGTC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lee, Se-Jin
APPLICANT: Esquela, Aurora F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1189 TATGTGTGGTATGGGCAGCCCAAGGTTGCATGGGAAAACACG 1230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AAAGAGAAGTCTTAACTGTGATCAGAACTCCAATCTGTGCTGTAGGAAAGACTATTATGT 186
                                                                                                                                                                                                                                      FILING DATE: 13-JUL-
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 CCACACCACGGTATTAAATCTCATTAAGGCCCAACA-----ATATCCAGACAGCAGTGAA 360
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                                                                 TELEPHONE: 619-678-5070
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                         NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/040001
                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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E: CA
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0; Mismatches 176;
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Best Local :
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GENERAL INFORMATION:
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            APPLICATION NUMBER: PCT/US95/
FILING DATE: 12-UUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1144 TGACATACCTGACATGGTAGTAGAGGCCTGTGGGTGCAGTTAG 1186
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                                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US95/08745
                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                904 TGGCTGGCACGACTGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCA 963
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TOPOLOGY: lir
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Local Similarity 65.3%;
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                  APPLICATION NUMBER:
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4225 Executive Square, Suite 1400
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1...357
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619-678-5099
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Pred. No. 1.6e-26;
                                                        07265/042WO1 (FD-3830)
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US-09-184-933-11
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Best Local (
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                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,933
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           APPLICANT: Lee, Se-Jin
APPLICANT: Esquela, Aurora F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1144 TGACATACCTGACATGGTAGTAGAGGCCTGTGGGTGCAGTTAG 1186
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LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 GGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGCAGCTAG 360
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               CLASSIFICATION:
                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 GGGATGGCGGGACTGGATACTGCAGCCCGAGGGGTACCAGCTGAATTACTGCAGTGGGCA 143
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OTHER INFORMATION:
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                                                                                                                                                                                          92037
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Similarity 65.3%;
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4225 Executive Square, Suite 1400
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; LOCATION:
US-09-184-933-11
                                                                                                                                                                                                                                                                                                                             Sequence 11, Application PC/TUS9508745
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO:
                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1144 TGACATACCTGACATGGTAGTAGAGGCCTGTGGGTGCAGTTAG 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1084 CACGGCCCGGCGCCCCTGTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGAC 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1024 CAATCTTCTCAAGGCCAACACAGCTGCAGGCACCACTGGAGGGGGCTCATGCTGTGTACC 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D. Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 GGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGCAGCTAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 TACTGCCCGAAGGCCCCTCTCTCTCCTCTACCTGGATCATAATGGCAATGTGGTCAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
                APPLICATION NUMBER: FILING DATE: 12-JUI
                                                                                      COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                         CITY: La JOlla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      964 GTGCCCACTACACATAGCAGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCT 1023
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                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                      COUNTRY:
CLASSIFICATION:
                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 CTGTGAGCCTGCGACCCCCTTATGTTGCAGGCGAGACCATTACGTAGACTTCCAGGAACT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 6.2%; Score 140.2; DB 3; Local Similarity 65.3%; Pred. No. 1.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/2
FILING DATE: 13-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCCCTCCCCACCTGGCTGGCAGCCCAGGCATTGCTGCCTCTTTCCATTCTGCCGTCTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGATGGCGGGACTGGATACTGCAGCCCGAGGGGTACCAGCTGAATTACTGCAGTGGGCA 143
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                                                                                                                                                                                        92037
                                                                                                                                                                                                           USA
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                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coding Sequence
1...357
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                                                                                                                                           Diskette
                12-JUL-1995
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                                 PCT/US95/08745
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                                                                                                                                                                                                                                                                                                       US-08-765-662-13; Sequence 13; Application US/08765662; Patent No. 5929213
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Best Local Similarity 65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 224; Conservative
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 360 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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NAME: Halle, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904 TGGCTGGCACGACTGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCA 963
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                                                                                                                                                                                                                                                                                                                                                                                                                               318 GGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGCAGCTAG 360
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                         STREET: 4225 E:
CITY: La Jolla
STATE: CA
                                                                                                   COUNTRY:
                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATCTTCTCAAGGCCAACAGCTGCAGGCACCACTGGAGGGGGGCTCATGCTGTACC 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCCTCCTCAAAGCCAACAATCCT-----TGGCCTGCCAGTACCTCCTGTTGTGTCCC 257
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                                                                                    CA
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                                                                                                                                                               E: Fish & Richardson
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                             THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE VENTION: GROWTH DIFFERENTIATION FACTOR-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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PCT-US95-08745-13

Sequence 13, Application PC/TUS9508745 GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish 6 KICHELDE...
STREET: 4225 Executive Square, Suite 1400

Fish & Richardson

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/
FILING DATE: 12-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
1228 GGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGCAGCTAG 1270
                                                                                                           1084 CACGGCCCGGCGCCCCCTGTCTCTCTCTATTATGACAGGGACAGCAACATTGTCAAGAC 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                     1144 TGACATACCTGACATGGTAGGTAGGCCCTGTGGGTGCAGTTAG 1186
                                                                                     1168 TACTGCCCGAAGGCCCCTCTCTCTCTCTACCTGGATCATAATGGCAATGTGGTCAAGAC
                                                                                                                                                                         1114 CAGCCTCCTCAAAGCCAACAATCCT-----TGGCCTGCCAGTACCTCCTGTTGTCTCCC 1167
                                                                                                                                                                                                                1024 CAATCTTCTCAAGGCCAACACACCTGCAGGCACCACTGGAGGGGGGCTCATGCTGTACC 1083
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                                                                                                                                                                                                                                                                                                                                             994 GGGATGGCGGGATACTGCAGCCCGAGGGGTACCAGCTGAATTACTGCAGTGGGCA 1053
                                                                                                                                                                                                                                                                                                                                                                                         904 TGGCTGGCACGACTGGATCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCA 963
                                                                                                                                                                                                                                                                                                                                                                                                                                   934 CTGTGAGCCTGCGACCCCCTTATGTTGCAGGCGAGACCATTACGTAGACTTCCAGGAACT 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             844 CTGCCAAGGAGGGTCCAGGATGTGCTGTCGACAAGAGTTTTTTGTGGACTTCCGTGAGAT 903
                                                                                                                                                                                                                                                                                                    964 GTGCCCACTACACATAGCAGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCT 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence LOCATION: 218...1267
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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                                                                                                                                                                                                                                                          GTGCCCTCCCCACCTGGCTGGCAGCCCAGGCATTGCTGCCTCTTTCCATTCTGCCGTCTT 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 140.2; DB 2; Length 2419; Pred. No. 3.6e-26;
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Search completed: October 11, 2002, 22:15:16 Job time: 64.7958 secs
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SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
6.2%; Score 140.2; DB 5; Length 2419;
Best Local Similarity 65.3%; Pred. No. 3.6e-26;
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NUMBER: PCT/US95/087
FILING DATE: 12-JUL-1995
                                                                      1084 CACGGCCCGGCCCCCCTGTCTCTGCTCTATTATGACAGCGACAGCAACATTGTCAAGAC 1143.
                                                                                                                                                                                                                               1114 CAGGCTCCTCAAAGCCAACAATCCT-----TGGCCTGCCAGTACCTCCTGTTGTGTCCC 1167
                                                                                                                                                                                                                                                         1024 CAATCTTCTCAAGGCCAACACACCTGCAGGCACCACTGGAGGGGGCTCATGCTGTGTACC 1083
                                                                                                                                                                                                                                                                                                              1054 GTGCCCTCCCCACCTGGCTGGCAGCCCAGGCATTGCTGCCTCTTTCCATTCTGCCGTCTT 1113
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., LISA A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042WO1 (FD-3830)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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COUNTRY: USA
COUNTRY: 92037
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TELEFAX: 619-678-5099
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 CAAGGAGCCATGCC
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B1986860 3183-03 M
BG801734 0114-08 M
BF455465 UI-M-BZ1-
BF455462 UI-M-BZ1-
                                                                      B1329959 602980519
BP533960 602075120
B1145698 602909842
B1148079 602912428
BF232704 602023292
BF533968 602075129
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BG566943 602589447
BI328115 602979264
BI246740 602959660
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11.7 11.7 11.7 11.7 11.7	111.8		12.0 12.0 12.0	12.1 12.1 12.1		122.3
358 603 348 714 583	631 285 443	586 475 443 390	537 522 549	346 506 347	513 376 568	404 440 585
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AA011197 AU143968 AW268442 BI861129 AA877215	BM272210 AA183246 BF109198 BF684212	AW209153 BE991905 AI201615 BF660636	BF791596 AI954151 BI499054	BE133911 BI695500 AA620486	BF062934 BI398655 BF151003 BF972653	BE852372 BE996475 BG684918 AZ795923
AAU11117 Ze235U1.5 AU143968 AU143968 AW268442 xv40b05.x B1861129 603390870 AA877215 ob15e02.s	0 1940f09 mt82907. 8 7158b11 2 6021411	AW209153 uc02f01.x BE991905 UI-M-BZ1- AI201615 qb81c01.x BF660636 maa82c06.	₽ 0	D C	BI39855 MIP-AVI- BI39855 MIP-AVI- BFJ51003 UY90h04.x BF972653 602243092	

ALIGNMENTS

		REMARK COMMENT	AUTHORS TITLE JOURNAL	KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 BC020693 LOCUS DEFINITION ACCESSION VERSION
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Tissue Procurement: CLONTECH CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	DSA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov	Strausberg, R. Direct Submission Direct Submission Submitted (03-JAN-2002) National Institutes of Health, Mammalian Submitted (03-JAN-2002) National Institutes, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive; Room 11A03, Bethesda, MD 20892-2590,	HTC. Human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1011)	BC020693 1011 bp mRNA linear HTC 22-JAN-2002 Homo sapiens, Similar to inhibin, beta C, clone IMAGE:4723762, BC020693

FEATURES SOUTCE

1. .1011

Location/Qualifiers

Series: IRAL Plate: 37 Row: g Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 15718678
This clone has the following problem: frame shifted.

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RESULT 2
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                                                                                                                                     TGCAGCTCCCTTCCAATACCACTTGGACCTTGAAAGTGAGAGTCCTTGTGCTGGGTCCAC 599
                                                                                                                                                                                                                                                                                           TCTCCTCTGATAGAACTGCTGGTGACAGGGAGGTCCAGCAGGCCAGTCTCATTGTTCTTTG 539
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                                                                                                                  AGCTGGTACTTGAAGGCCAGGTAGCCCAGAGCTCA 754
                                                                                                                                                                                                            ACCTCCACGGGGTCCCACAGGGGGCACTTCTAGAGGACACAGGGAACAGGGAATGTGAAA 419
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                    602589447F1 NIH_MGC_76 Homo sapiens
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          mRNA sequence.
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276 c 243 g 22
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/tissue_type="Liver"
/clone_lib="NIH_MGC_76"
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/db_xref="taxon:9606"
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                        CCCAGCGCCCAACACTGAACCGCCCTGTGTCCAGAGCTGCTTTTGAGGACTGCACTGCAGC
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ACCTCCACGGGGTCCCACAGGGGCACTTCTAGAGGACAACAGGGAACAGGAATGTGAAA 436
                                                                                           CCCGGCGCCCAACACTGAACCGCCCTGTGTCCAGAGCTGCTTTGAGGACTGCACTGCAGC
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Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1583 row: m column: 11 High quality sequence stop: 539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_1ib="NMGE_1723762"
/clone_1ib="NHGE_1723762"
/clone_1ib="NHIB_KGT_76"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="NHIB (Clontech); Site_1:
Sit (ggcqsctcggc; Site_2: Sfi (ggcqattatggcc); 5' and
3' adaptor sequence:
5' -Adaptor sequence:
5' -ATTCTAGAGGCGGCGACATG-dT[30]BN-3' (where B - A,
C, or G and N - A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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                                                                                                                                                                                                                                     121
   276 GCATCTTGGACAAGCTGCACCTCACCCAGCGCCCAACACTGAACCGCCCTGTGTCCAGAG,335
                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGCTTCTGGCCTTTC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGTCCCTGGTGCCCAGGACAGAGTTGAAGCCACTCCCGTTGAGACCCTGAATATAGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGCCTCTGGCAGCCAGGACAGAGTTGAGACCACAGCTGTTGAGACCCTGAGCCCTGAG 95
                                                                               GCCCTGCCATCTTTGACCTGGAGAGCCAGCGGGAGCTGCTTCTCGATTTGGCCAAGAAAA 240
                                                                                                                  GGGGGCCCACCTTGGAACTGGAGAGCCAGCGGGAGCTGCTTCTTGATCTTGGCCAAGAGAA 275
                                                                                                                                                                                                                                     TGTTCCTGACTCCAACCACAGTAGTGAACCCCCAAAACTGAGGGTCCATGCCCAGCATGTT 180
                                                                                                                                                                                                                                                                                                                TCCTCCTGGCTCCAACCACACTGGCCACTCCCAGAGCTGGCGGTCAGTGTCCAGCATGTG 215
                                                                                                                                                                                                                                                                                                                                                                                            TTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTCCTTGCTCCTGGCTCTTC 120
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BI328115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI1324 row: o column: 16
High quality sequence stop: 758.
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Tissue Procurement: Jeffrey E. Green, M.D.
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/clone="IMAGE:5132391"
/clone="IMAGE:5132391"
/clone="NGI_CGAP_L19"
/clone="NGI_CGAP_L19"
/lab_bost="0H10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: liver; NotI; Not
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/strain="FVB/N"
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Pred. No. 1.9e-55;
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RESULT 4
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ATGACCAGAGACAAGAAGAATATGAGATCATCAGCTTTGCTGACACAGACCTCTCCAGCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 CTGCTTTGAGGACTGCACCTGCAGCGGGGTCCCACAGGGGGCACTTCTAGAG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GGGCTCTCAAGACCGCGCTGCAGCGCCTCCGCGGGCCTCGACGGGAAACCCTGTTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      752 TCAGTCATCCTGGG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTGGAGGTGGATGGCAGTGGCTGGCATCAACTCCCCCTAGGGCCTGAAGCTCAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATAAGAGTTCTTGTGCTAAGACCATATGACACCAACCTCACCTTGACAAGTCAGTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GACAACAGGGAACAGGAATGTGAAATCATCAGCTTTGCTGAGACAGGCCTCTCCACCA 452
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                                                                                                                                                                                                                                            plate: Liamili306 row: g column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI246740.1 GI:14790995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 893)
/clone_lib="NCI_GGAP_L19"
/lab_host="0H10B (Tl phage=resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
                                                                                                             /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5125287"
                                                                                                                                                                                   /organism-"Mus musculus"
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 5
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                        DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                                                                                                CATCCAGCCTGAGGGCTACGCC 943
                                                                                                                                                                                                                                                                            CATCCCAGCTTGAGGATATGCC 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTGCAGCCAGGGCACCTGACCCTGG-AGCTGGTACTTGAAGGCCAGGTAGCCCA-GA 749
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                Mus mus
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AUTHORS
TITLE
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                                                 441 GCCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTTCTCCTCTGATAGAACTGCTG
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                                                                                                                                                                                                                                                                       324 CTGTGTCCAGAGCTGCTTTGAGGACTGCACTGCAGCACCTCCACGGGGTCCCACAGGGGG
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ACCTCTCCAGCATCAACCAGACCGGCTCGAGTTCCACTT---CTCTGGTAGAATGGCCA
                                                                                                                                   CACTTCTAGAG----GACAACAGGGAACAGGAATGTGAAATCATCAGCTTTGCTGAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGGCTCTTCTGTTCCTGACTCCAACCACAGTAGTGAACCCCAAAACTGAGGGTCCAT
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can i
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1327 row: f column: 06
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National Institutes of Health, Mammalian
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    Mismatches

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Pred. No. 2e-53;
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                                              CTGGTGCCCAGGACAGAGTTGAAGCCACTCCCGTTGAGACCCTGA-ATATAGGCTTGGGT 63
    TGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGCTTCTGGCCTTTCTCCTCCT 162
                                                                                            CTGGCAGCCAGGACAGAGTTGAGACCACAGCTGTTGAGACCCCTGAGCCCTGAGTCTGTAT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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BF533960
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Tissue Procurement: Jeffrey E. Green, M.D.
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National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                          Conservative
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/db_xref="taxon:10090"
/clone="IMAGE:4212125"
/clone=lib="NCI_CGAP_Li9"
/clone=lib="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pcMV-SPORT6; Site_1: NotI;
/note="organ: liver; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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COMMENT DEFINITION SOURCE VERSION ACCESSION rocus REFERENCE KEYWORDS AUTHORS TITLE ORGANISM JOURNAL' Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 841) Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Unpublished (1999) Contact: Robert Strausberg, Ph.D. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) BI145698.1 GI:14605699 mRNA sequence 602909844F1 NCI_CGAP_Li9 Mus house mouse musculus cDNA clone IMAGE:5050810 mRNA EST 05-JUL-2001

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DEFINITION
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mRNA sequence.
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                                                  BI148079 941 bp mRNA linear EST 05-JUL-602912428F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5053471
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/lab_host="DHIOB (Tl phage-resistant)"
/note="Organ: liver; Vector; pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/clone="IMAGE:5050810"
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Pred. No. 1.6e-52;
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                                                                           1066 GGGCTCATGCTGTGTACCCACGGCCCGGGCGCCCCTGTCTCTGTCTCTATTATGACAGGGA 1125
                                                                                                                                                                                     1006 CTTTCACACTGCAGTGCTCAATCTTCTCAAGGCCAACACAGGTGCAGGCACCACTGGAGG 1065
                                            419 GGGCTCGTGCTGCGTGCCTACATCTCGGCGCCCTCTGTCTTTGCTCTACTATGACAGGGA 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 -CACCTTACTCTGGAGCTGGTACCAGAAAGCCAGGTGGCCCACAGTTCCTTGATCCTGGG
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                                                                                                                                                                                                                                  CGTAGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTATGCCAT
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CDNA Library Areparation: Life Technologles, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
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plate: LLAMIl145 row: g column: 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 941)
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/db_xref="taxon:10090"
/clone="rMAGE:5053471"
/clone=lib="NCI_CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally, Primer: Oligo dT
Average insert size 1.9 kb, Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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83.98;
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Pred. No. 4.3e-52;
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                                                                                                                                                                                                                                                                                                    CCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGCTTCTG 148
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AAGAAAAGTATCCTGGACAAGCTGCACCTCAGCCAGCGCCCCATACTCAGTCGGCCAGTG
                       AAGAGAAGCATCTTGGACAAGCTGCACCTCACCCAGCGCCCAACACTGAACCGCCCCTGTG 328
                                                                                     GCATGTTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGAGCTGCTTCTCGATTTGGCC
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                                                                                                                                                                     GCTCTTCTGTTCCTGACTCCAACCACAGTAGTGAACCCCCAAAACTGAGGGTCCATGCCCA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrange by: The M.A.G.E. Consortium (LLNL)
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:10090"
/db_xref-"taxon:10090"
/clone="IMAGE:4158766"
/clone="IMAGE:4158766"
/clone="IMAGE:4158766"
/clone="IDH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT:
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT:
/sylverage insert size 1.9 kb. Constructed by Life
/rechnologies. Note: this is a NCI_CGAP Library."

a 253 c 221 g 175 t
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Pred. No. 2.8e-49;
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602075129F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4212175
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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1 (bases 1 to 975)
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                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                         quality sequence stop: 659
/OLGAINSWETTENDYN"
/Strain="TVB/N"
/db_xref="TVB/N"
/clone="TWAGE:4212175"
/clone="IMAGE:4212175"
/clone="IMAGE:4212175"
/clone="IMAGE:4212175"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 297 c 266 g 222 t
                                                                                                                                                                                                                              /organism="Mus musculus"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TGTTCCTGACTCCAACCACAGTAGTGAACCCCAAAACTGAGGGTCCATGCCCAGCATGTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 TCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGCTTCTGGCCTTTC 155
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Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Liu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma
                                                                                                                                                                                                                                                                  AV658436 GLC Homo sapiens cDNA clone GLCFME02 3', mRNA sequence.
                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                            Homo sapiens
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mmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
(bases 1 to 594)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tlssue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                             1113 bp AGENCOURT_6445395 NIH_MGC_72 Homo 5', mRNA sequence.
                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1113)
                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                Unpublished (1999)
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                           BM463852.1 GI:18512894
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Tel: 86-21-50801919(ex.45)
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Chinese National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hanzg@chgc.sh.cn
This clone is available at CHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, zhangjiang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.5e-34;
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Plate: LLAM12235 row: a column: 03
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Kargul, G.J., Dudekola, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka T.S., Carter, M.G. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       H3101G11-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3101G11 5', mRNA sequence.
BG084513
                  National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelysun.grc.nla.nlh.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nla.nlh.gov/cDNA/15k.html for details. Plate: H3101 row: G column: 11
Seq primer: -21M13 Reverse
                                                                                                                                                                   Unpublished (2001)
Other_ESTs: H3101G11-3
Contact: George J. Kargul
Laboratory of Genetics
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                                                                                                                                                                                                                                                  Verification and initial annotation of NIA mouse 15K cDNA clone set
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI:
Site_2: SalI: Cloned unidirectionally. primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
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201 c 262 g 292 t 7 others
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                      викатуота; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Nammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W
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Mol Genet 7: 1967-1978."
1 73 c 112 g 134 t
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/db_xref="niaEST:H3101G11-5"
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Matches 280; Conservative
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                                                                               Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA Tel: 713 792 3646
Fax: 713 790 0329.
                                                                                                                                                                                         and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
Contact: Klein WH
                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosťomį;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mds.
1 (bases 1 to 567)
1 (bases 1 to 567)
Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
Mu,X., Zhao,S., Pershad,R.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
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0114-08 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
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Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
BOX 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
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/organism="Mus musculus"
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/dlone_lib="Mouse_E14.5 retina_lambda_ZAP_II_Library"
/tissue_type="neural retina"
/dev_stage="embryonic_day_14.5 post-fertilization"
/dev_stage="embryonic_day_14.5 post-fertilization"
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           CTGTTTAAGCTGCAGTAACTTTTCTGACTATGGATCATCGTTCCTT 2272
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/tissue_type="neural retina"
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Search completed: October 12, 2002, 02:04:45
Job time: 1861.4 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Best Local
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     EP1074620-A1
                                                                                                                                                                       Human; transforming growth factor-beta; monomeric protein; MP52; MP121; dimeric protein; TGF-beta; vulnerary; antiulcer; nootropic; neuroprotective; antiinfertility; osteopathic; gene therapy; bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A cDNA library prepared using total RNA from human liver was subjected to PCR amplification using primers corresp. to conserved regions within the TGF beta family. Amplification products were subcloned and sequences; one clone (designated pSK-MP121) was found to contain a new sequence. Part of the insert from the clone was used to re-screen the human liver cDNA library and a 2272 bp fragment coding for a TGF-beta-like protein (i.e. the present sequence) was isolated. This protein has mitogenic and differentiation-inducing properties making it (or fusion proteins comprising it or heterodimers of the protein with a cystine knot motif protein) useful for inducing tissue regeneration, e.g. for wound healing, inducing growth of the protein with a cystine knot motif protein inducing fortains.
                                                                       Misc-difference
                                                                                                                                                              cartilage; dental; wound healing; connective tissue
                                                                                                                                                                                                                                                          Human TGF-beta MP121
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                 08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                   AAB70530 standard; Protein; 352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 11; 15pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatic tissue or bone marrow precursor cells, treating fertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DRTAGDREVOQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTSSLLLAFLLLAPTTYATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation-inducing activity, e.g. for use in wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding transforming growth factor beta MP-121 - has mitogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                            (first entry)
                                                                         Location/Qualifiers 316
                                                    /note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1849; DB 17; 100.0%; Pred. No. 3.1e-171;
                                                                                                                                                                                                                                                      protein sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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121

61 ш

121 DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL 180

DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL

180

PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS 120

PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS

PLGPEAQAACSQCHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGIDC

PLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGIDC

241 QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN 300

QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN

300

Matches Query Match

351;

Conservative

0,

Indels Length 352;

0;

Gaps

0;

Local

Similarity

99.48; 99.78;

Score 1838; DB 22; Pred. No. 3.6e-170; Mismatches

1 MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60

MTSSLLLAFILLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR

60

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CC indicated. Diseases treatable include diseases associated with bone CC and/or cartilage damage or affecting bone and/or cartilage disease or CC situations in which cartilage and/or bone growth is desirable, for spinal CC fusion, for damaged or diseased tissue associated with connective tissue CC including tendon and/or ligament, periodontal or dental tissue including CC dental implants, neural tissue including CNS tissue and neuropathological CC situations, tissue of the sensory system, liver, pancreas, cardiac, CC blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane, CC tissue regeneration, angiogenesis, wound healing including ulcers, burns, CC tissue regeneration, angiogenesis, wound healing including ulcers, burns, CC or bone marrow cells, for maintenance of a state of proliferation or CC differentiation, for treatment or preservation of tissue or cells for organ or tissue transplantation, for integrity of gastrointestinal lining CC and for treatment of disturbances in fertility, contraception or pregnancy. The present sequence represents the specifically claimed CC TGF beta monomeric protein MPI21, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a protein (I) selected from the members of the transforming growth factor-beta (TGF-beta) superfamily, which is monomeric due to substitution or deletion of a cysteine which is responsible for dimer formation. Also described are: (1) nucleic acid (II) encoding (I); (2) expression vector (III) containing (II) in a suitable vector system; (3) host cell (IV) containing (III) capable of producing (I); and (4) a pharmaceutical composition (V) containing (I), (III) or (IV). (I) has vulnerary, antiulcer, nootropic, neuroprotective, antiinfertility and osteopathic activities, and can be used in gene therapy. (V) is useful for the prevention or therapy of diseases for which also the dimeric form of the protein would be indicated with the content of the protein would be
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel monomeric protein of transforming growth factor-beta family for prevention or therapy of diseases associated with bone, cartilage damage, promotion of wound healing, has substitution or deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 21-22; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF74421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 2001-228100/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1999;
352 AA;
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AAW60617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoas; menstrual disorder; transgenic; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liver activin; beta c; beta e; cell differentiation; haematopoiesis; erythroid; ovarian follicular maturation; hormone; neuronal survival;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine liver activin beta c polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW60617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW60617 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
This represents a murine liver activin beta c polypeptide. Sequences derived from beta c cDNA clone is used for screening and cloning a liver activin beta e gene. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopolesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders
                                                                                                                                                                                                                                         WPI; 1998-312408/27.
N-PSDB; AAV38237.
                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9822492-A1
                                                                                                                                                                                                                                                                                   Bonadio J,
                                                                                                                                                                                                                                                                                                                                          20-NOV-1996;
                                                                                                                                                         Claim 16; Fig 1; 141pp; English.
                                                                                                                                                                                                                                                                                                               (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                   Fang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-
173..1
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111..113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Asn is putatively N-glycosylated"
21..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "endoproteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "propeptide domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Asn is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "mature growth factor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putatively N-glycosylated"
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AAR92754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, or the transgenic animals, are useful for screening for liver activin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulators.
                                                                                                                                                                                                                                                                                               Growth differentiation factor-12; GDF-12; liver; cell proliferation; cancer; diagnosis; therapy; transforming growth factor beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR92754 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                     Human growth differentiation factor-12.
                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1996 (first entry)
                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 G-RMASGMEVROTREMEEVOEPHNATOTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYO
                                                                                      W09602559-A1
                                                                                                                                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PILSRPVSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MASSLLLALLELTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTLNRPVSRAALRTALQHLHGVPQGALLE-DNREQECEIISFAETGLSTINQTRLDFHFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COGASRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGOCPLHIAGMPGIAASFHTAVL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
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                                                                                                                                                        /label- N-glycosylation_site 232..236 237..350
                                                                                                                        /note= "GFR-12 active
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.3%;
75.9%;
                                                                                                                                          C-terminal_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1392; DB 19;
Pred. No. 8.5e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                          C-terminal fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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12-JUL-1995;

95WO-US08745

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                Human; full length cDNA; cDNA synthesis; oligo-capping.
                                          Homo sapiens
                                                                                                                                  06-NOV-2001 (first entry)
              EP1130094-A2
                                                                                                      Human polypeptide,
                                                                                                                                                                    AAM93672;
                                                                                                                                                                                            AAM93672 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             member of the transforming growth factor beta superfamily that is expressed specifically in liver. It can be obtd. by expression of a cDNA clone (AAT16883) derived from adult liver in transformed host cells. GDF-12 possesses activities that will make it useful in the treatment of liver disorders, e.g. disease states in which liver function is compromised, or cellular proliferative disorders such as hepatocellular carcinoma. In can also be used to expand liver cells in culture and to raise diagnostic antibodies.
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human growth differentiation factor-12 (GDF-12 - AAR92754) is a new
                                                                                                                                                                                                                                                                                                                                                                                                                      184 PEAQAACSQGHLTLEL---VLEGQ---VAQSSVILGGAAH-RPFVAARVRVG--GKHQIH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 40-43; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferative disorder of liver origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding Growth Differentiation Factor-12 - used in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 HLYHARLWLHV-LPT-LPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL---GWHTLTLP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 EVQQASLMFFVQLPSNTTWTLKVRVLVLGP----HNTNLTLATQYLLEVDASGWHQLPLG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT16883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED
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13-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 QAALTRALRRLQ----PGSVAPGNGE----EVISFATVTDSTSAYSSLLTFHLSTPRS----H 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 RAALRTALOHLHGVPOGALLEDNREQECEIISFAE-TGLSTINOTRLDFHFSSDRTAGDR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 WLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPB 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 FLLLAPTTVATPRAGGOCPACGGPTLELESORELLLDLAKRSILDKLHLTORPTLNRPV6 68
                                                                                                                                                                                                                                                                                                                              RRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASF 294
                                                                                                                                                                                                                                                                                                                                                                                        SSGLRGEKSGYLKLQLDCRPLEGNSTYTGQPRRLLDTAGHQQPFLELKIRANEPGAGRAR,
                                                                                                                                                                                                                                                                                                                                                           RRGIDCQGGSRMCCRQEFFYDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapeutic methods esp. in methods for treating a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1996-105850/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee S;
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94US-0274215
                                                                                                      SEQ ID NO: 3558.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 664; DB 17; Length 3 Pred. No. 5.1e-56; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 350;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clones. 80 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                       295
                                                                       295
                                                                                                                                                                                                              175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to primers for synthesising full length CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 3558; 1380pp + sequence listing; English.
                                                                                                                                        235
                                                                                                                                                                                                                                 184 PEAQAACSOGHLTLEL---VLEGQ---VAQSSVILGGAAH-RPFVAARVRVG--GKHQIH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                   120 HLYHARLWLHY-LPT-LPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL---GWHTLTLP
                                                                                                                                                                                                                                                                                                     128 EVQQASLMFFYQLPSNTTWTLKVRVLVLGP----HNTNLTLATQYLLEVDASGWHQLPLG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                         69 QAALTRALRRLQ---PGSVAPGNGE---EVISFATVTDSTSAYSSLLTFHLSTPRS---H 119
                                                                                                                                                                                                                                                                                                                                                                         69 RAALRTALQHLHGVPQGALLEDNREQECEIISFAE-TGLSTINQTRLDFHFSSDRTAGDR 127
                                                                                                                                                                                                                                                                                                                                                                                                          9 WLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                  9 FLLLAPTTVATPRAGGOCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVS 68
                                                                                                                              HSAVFSLLKANNPWPAST----SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS
                                                                                        HTAYLNLLKANT--AAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEACGCS 352
                                                                                                                                                                                                SSGLRGEKSGVLKLQLDCRPLEGNSTVTGQPRRLLDTAGHQQPFLELK1RANEPGAGRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in genetic manipulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0194486.
2000JP-0118774.
2000JP-0183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.9%; Score 664; DB 22; 43.3%; Pred. No. 5.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Hayashi K, I;
na T, Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
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AAW60619; 01-FEB-1999

(first entry)

AAW60619 standard; Protein; 350

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                                                       Matches 154;
                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human liver activin beta e polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                        liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopoiesis, particularly erythropolesis, for treating haemorphila, cystic fibrosis or menstrual disorders. Antibodies are useful in cystic fibrosis or menstrual disorders antibodies (which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic administrative activin giver activin modulators.
                                                                                                                                                                                                                                                                                                                                                                        secretion, negative morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat the compound of expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopoiesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This represents a human liver activin beta e polypeptide. The invention provides murine beta c and beta e polypeptides and the encoding genes, bisorders of cell growth or differentiation (or susceptibility to them).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNMI ) UNIV MICHIGAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 5; 141pp; English.
                                                                                                                                       Sequence
                9 FLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVS 68
                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-312408/27.
                                                                                                                                       350 AA;
                                                           Conservative
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237..3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 350
                                                                         35.4%; Score 655; DB 19; Length 350; 42.8%; Pred. No. 3.9e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "endoproteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "mature growth factor domain"
                                                             54;
                                                             Mismatches
Indels
                                                                                                                                                                                                                                             transgenic animals
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 AAW60618 standard; Protein; 350
                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay; menstrual disorder; transgenic; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liver activin; beta c; beta e; cell differentiation; hacmatopoiesis; erythroid; ovarian follicular maturation; hormone; neuronal survival;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine liver activin beta e polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1999
                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp
Claim 16; Fig 2; 141pp; English
                       New isolated nucleic acid encoding sub-units of liver activin useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders
                                                                                                                                                                              20-NOV-1996;
                                                                                                                                                                                                          20-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                             Modified-site
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                                                                                                                         Bonadio J,
                                                                               N-PSDB; AAV38238
                                                                                                                                                 (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 WLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILEGLHLTSRPRITHPPP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSGLRGEKSGYLKLQLDCRPLEGNSTYTGQPRRLLDTAGHQQPFLELKIRANEPGAGRAR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAQAACSQGHLTLEL---VLEGQ---VAQSSVILGGAAH-RPFVAARVRVG--GKHQIH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLYHARLWLHV-LPT-LPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL---GWHTLTLP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAALRTALOHLHGVPQGALLEDNREQECEIISFAE-TGLSTINQTRLDFHFSSDRTAGDR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQQASLMFFVQLPSNTTWTLKVRVLVLGP----HNTNLTLATQYLLEVDASGWHQLPLG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAAVTRALRRLQ---PGSVAPGNGE---EVISFATVTDSTSAYSSLLTFHLSTPRS---H 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGGPGIAASF
                                                                                                                        Fang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                              96US-0752919
                                                                                                                                                                                                          97WO-US20882
                                                                                                                                                                                                                                                                                                        /note=
237..3
                                                                                                                                                                                                                                                                                                                                                                                            22..236
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                198..200
                                                                                                                                                                                                                                                                                                                                                                          /note- "propeptide domain"
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "signal sequence"
                                                                                                                                                                                                                                                                                                         . 349
                                                                                                                                                                                                                                                                                          "mature growth factor domain"
                                                                                                                                                                                                                                                                                                                     "endoproteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                 "Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ⋛
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RESULT 8
AAY92017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aturation, hormone secretion, neuronal survival, spermatogenesis, bone of commetion, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and compound or agent that upregulates the compound's expression. Antagonists of increase growth and regeneration of liver tissue. The liver activin occumpound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopolesis, particularly erythropolesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which to liver activin receptors) and to inhibit liver activin. Also, the stransgenic animals containing liver activin gene can be used to produce or the transgenic animals, are useful for screening for liver activin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Homo sapiens
                                                                                   human inhibin B beta subunit; CKGF; mutant; cystine knot growth factor;
                                                                                                                                                 Human inhibin B beta subunit.
                                                                      hairpin loop;
                                                                                                                                                                                                   19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                        AAY92017 standard; Protein; 407
                                                                                                                                                                                                                                                               AAY92017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 S 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 TLPSSGLRSEDSGYVKLQLEFRPLDLNSTAAGLPRLLLDTAGQQRPFLELKIRANEPGAG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of haematopolesis, erythroid differentiation, ovarian follicular
                                                                                                                                                                                                                                                                                                                                                                                                                                          350 S 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 ASFHSAVFSLLKANNP--WPAGSSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 ASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 RARRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 QIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PLGPEAQAACSQGHLTLELVLEGQVAQSS-----VILGGAA-HRPFVAARVRVG--GKH 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 TAGDREVQOASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLE--VDASGWHQL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 PLPQAALTRALRRLQ--PK-SMVPGNRE---KVISFATIIDKSTSTY-RSMLTFQLS--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LLAFILLAPTTVATPRACGOCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLWSHHLYHARL -- WLHVPPSFPGTLYLRIFRCG -- TTRCRGFRTFLAEHQTTSSGWHPL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVSRAALRTALQHLHGVPQGALLEDNREQECETISFA---ETGLSTINQTRLDFHFSSDR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWLILLWALVWYQSRRSA--CPSCGGPTLAPQGERALVLELAKQQILEGLHLTSRPRITR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                        infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%; Score 648; DB 19; Length 350; 42.4%; Pred. No. 1.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118;
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                                                                                                                                               Query Match
                                                                                                                                                                                                                                                          mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological mutant transformations.
                                                                                                                                                                                Sequence
                                                                                                                                                                                                        Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mutants comprise at least one electrostatic charge altering mutation in beta hairpin loop, resulting in increased bloactivity.

Mutant cystine knot growth factor (CKGF) proteins comprising one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the wild type human inhibin B beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 298; Page 304; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-283585/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weintraub BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 401..407
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54 KLHLTQRPTLNRPVSRAALRTALQHLHGVPQGALLEDNR-----
                                    29 SPTPPPTPAAPPPPPPPGSPGGSQDTCTSCGG----FRRPEELGRVDGDFLEAVKRHILS 84
                                                                     13 APTTVATPRA------GGQ----CPACGGPTLELESQREL------LLDLAKRSILD 53
                                                                                                                                Local
                                                                                                                              Similarity
                                                                                                                                                                                  407 AA;
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Szkudlinski MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US19772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= beta_hairpin_loop_1
/note= "mutant optionally comprises one |
substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376..400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "mutant optionally comprises one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= beta_hairpin_loop_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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interaction between beta hairpin structure an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                            32.4%; Score 599.5; 36.6%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interaction between beta hairpin structure and
a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nteraction between beta hairpin
                                                                                                            60;
                                                                                                         Mismatches 118;
                                                                                                                            No. 1.2e-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between beta hairpin structure and
                                                                                                                                          DB 21;
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                                                                                                       Indels
                                                                                                                                          Length 407
     ----EQEC 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY92019 standard;
                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                               Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human activin B subunit; CKGF; mutant; cystine knot growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human activin B subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hairpin loop; infertility.
                                                                                                                                                                                                                    Misc-difference 401..407
WPI; 2000-283585/24
                         Weintraub BD,
                                                                            22-SEP-1998;
                                                                                                                              30-MAR-2000.
                                                                                                                                                      WO200017360-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 KVRVLVL---GPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQV 205
                                                                                                     19-MAR-1999;
                                                  (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 RLQMRGRPNITHAVPKAAMVTALRKLHA---GKVREDGRVEIPHLDGHASPGADGQERVS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQELAYVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQSSVIL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFRE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVRVKVYFQEQGHGDRWNM-VEKRVDLKRSGWHTFPLTEAIQALFERGERRLNLDVQCDS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIISFAETDGLASSRVRLYFFISNE---GNQNLFVVQASLWLYLKL---LPYVLEKGSRR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIISFAETGLSTINQTRLDFHFSSDRTAGDRE--VQQASLMFFVQLPSNTTWTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR----GLNPGTVNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                         Szkudlinski MW;
                                                                            98WO-US19772.
                                                                                                     99WO-US05908
                                                                                                                                                                                                                                                                                                                            329..375
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..307
                                                                                                                                                                               /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure and
a receptor"
                                                                                                                                                                                                                                /label= beta_hairpin_loop_3
/note= "mutant optionally comprises one or more
substitutions in these residues"
                                                                                                                                                                                                                                                                        376..400
                                                                                                                                                                                                                                                                                /label= beta_hairpin_loop_1
/note= "mutant optionally c
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                           interaction between a receptor"
                                                                                                                                                                                                                                                                                                                                        substitutions in these residues"
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 145; Conservative 60; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bloactivity.

Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factor: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g. hypothyroidism and thyroid cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the wild type human activin B subunit.
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                                                                                                                               09-APR-1991
                                                                                                                                                                            AAP70204;
                                                                                                                                                                                                                      AAP70204 standard; protein;
                                        Fertility control;
                                                                                     Sequence of human inhibin beta-chain precursor beta-B
                                                                                                                                                                                                                                                                                                                                372 CIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 IGWHDWIIQPEGYAMNECIGQCPLHIAGMEGIAASFHTAVLNLLKANTAAGTTGG--GSC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 KVRVKVYFQEQGHGDRWNM-VEKRVDLKRSGWHTFPLTEAIQALFERGERRLNLDVQCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 KVRVLVL---GPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 EIISFAETDGLASSRVRLYFFISNE---GNQNLFVVQASLWLYLKL---LPYVLEKGSRR 195
                                                                                                                                                                                                                                                                                                                                                                          317 CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 CQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFF1DFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 AQSSVIL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFRE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 KLHLTQRPTLNRPVSRAALRTALQHLHGVPQGALLEDNR------EQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 SPTPPPTPAAPPPPPPPGSPGGSQDTCTSCGG----FRRPEELGRVDGDFLEAVKRHILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 APTTVATPRA------GGQ---CPACGGPTLELESOREL-----LLDLAKRSILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 EIISFAETGLSTINQTRLDFHFSSDRTAGDRE--VQQASLMFFVQLPSNTTWTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLQMRGRPNITHAVPKAAMVTALRKLHA---GKVREDGRVEIPHLDGHASPGADGQERVS 141
                                                                                                                                                                                                                                                                                                                                                                                                                     IGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR---GLNPGTVNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 AA;
                                                                                                                               (first entry)
                                            contraception;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.4%; Score 599.5; DB 21; 36.6%; Pred. No. 1.2e-49;
                                            hormone;
                                            spermatogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed an immodulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1987-137512/20
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03-OCT-1985;
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                                                          227
                                                                                                                      167
                                                                                                                                                                                            123 TAGDRE--VQQASLMFFVQLPSNTTWTL-----KVRVLVL----GPHNTNLTLATQYLLE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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Modified-site
j
                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                           80 HGVPQGALLEDNR-----
                                                                                                                                                                                                                                                                                                                            26 CPACGGPTLELESQREL-----LLDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQHL 79
                                                                                                                                                                                                                                                                                                                                                                                    ocal
                                                                                                                                                                         --GNQNLFVVQASLWLYLKL---LPYVLEKGSRRKVRVKVYFQEQGHGDRWNM-VEKRVD
      AGMPGIAASFHTAVLNLLKANTAAGTTGG--GSCCVPTARRPLSLLYYDRDSNIVKTDIP 342
                                                  RIGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYL
                                                                                                             LKRSGWHTFPLTEAIQALFERGERRLNI.DVQCDSCQELAVVPVFVDPGEESHRPFVVVQA 226
                                                                                                                                          VDASGWHOLFLGPEAQAACSQGHLTLELVLEGQVAQSSVIL-----GGAAHRPFVAARV 225
                                                                                                                                                                                                                                                                                                CTSCGG----FRRPEELGRVDGDFLEAVKRHILSRLQMRGRPNITHAVPKAAMVTALRKL 56
                                                                              RVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHI 284
                                                                                                                                                                                                                               HA---GKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSRVRLYFFISNE, 112
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               353 AA;
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85US-0906729.
85US-0783910.
86US-0827710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="used to design a long synthetic DNA probe" 238..343 235..237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="proteolytic processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="potential N-linked glycosylation sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 38..40
                                                                                                                                                                                                                                                                                                                                                                               31.9%;
                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                 ------EQECEIISFAETGLSTINQTRLDFHFSSDR 122
                                                                                                                                                                                                                                                                                                                                                                            Score 590; DB 8;
Pred. No. 8.1e-49;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                113;
                                                                                                                                                                                                                                                                                                                                                                                          Length 353;
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17

44 LDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQHLHGVPQGALLEDNR-------

LEAVKRHTLNRLQMRGRPNITHAVPKAAMVTALRKLHA---GKVREDGRVEIPHLDGHAS

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   Matches
                         Query Match
                                                                               mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
                                                                                                                                         A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the
                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1986;
03-OCT-1985;
10-FEB-1986;
                                                 Sequence
                                                                                                                                                                                                                                                        Recombinant human or porcine inhibin or activin modulating clinical condition or reproductive pl
                                                                                                                                                                                                                   Disclosure; Fig 2B; 48pp; English.
                                                                                                                                                                                                                                                                                           N-PSDB; AAN70318.
                                                                                                                                                                                                                                                                                                                                Mason
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fertility control; contraception; hormone; spermatogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of porcine inhibin beta-chain precursor beta-B.
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                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP70201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP70201 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343
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               Local
                                                                                                                                                                                                                                                                                                       1987-137512/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGVPGSASSFHTAVVNQYRMR----GLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVP 343
                                                                                                                                                                                                                                                                                                                                ٦ď,
               Similarity
                                                 351 AA;
                                                                                                                                                                                                                                                                                                                             Seeburg PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domestica
 31.3%;
llarity 37.3%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                          86US-0906729.
85US-0783910.
86US-0827710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AA
            Score 578;
Pred. No. 1
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              processing site"
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            DB 8;
.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               long synthetic DNA probe"
  111;
                                                                                                                                                                                                                                                     in - used for physiology of
                       Length 351;
Indels
                                                                                                                                                                                Also claimed
42;
Gaps
9
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RESULT 12
AAP70200
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03-OCT-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP70200 standard; protein; 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fertility control; contraception; hormone; spermatogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of porcine inhibin beta-chain precursor beta-A.
                                                                                                                                                                 Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of . 
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                                                                                                                                                                                                                                                                                                                                                                     02-OCT-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
              chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or
                                                                  A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
                                                                                                                                                        animals.
                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                       Mason AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
prodomain immunogens are useful in
                                                                                                                           Disclosure; Fig 2B; 48pp; English.
                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVQCDGCQELAVVPVFVDPGEESHRPFVVVQARLGDSRPHRIRKRGLECDGRTNLCCRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLEGQVAQSSVIL-----GGAAHRPFVAARVRVGGK--HQIHRRGIDCQGGSRMCCRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EQECEIISFAETGLSTINQTRLDFHFSSDRTAGDRE--YQQASLMFFYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TV--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN--LLKANTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEKGSRRRVRVKVYFQEPGHGDRWDVVEKRVDLKRSGWHTLPLTEAIQALFERGERRLNL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGADGQERVSEIISFAETDGLASSRVRLYFFISNE---GNQNLFVVQASLWLYLKLLPYV 130
                                                                                                                                                                                                                            1987-137512/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFIDFRLIGWSDWIIAPTGYYGKYCEGSCPAYLAGYPGSASSFHTAVVNQYRMRGLNPFG
                                                                                                                                                                                                                AAN70317
                                                                                                                                                                                                                                                       Seeburg PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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85US-0783910.
86US-0827710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="used to design a long synthetic DNA probe" 309.424 304.308
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1..308
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="proteolytic processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ
 monitoring preproinhibin
                                                                        Also claimed :
inhibin-beta • :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251
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                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                            Fertility control; contraception; hormone;
                                                                                                                                                                                                                                                                                     Sequence of human inhibin beta-chain precursor beta-A.
                                                                                                                                                                                                                                                                                                                  09-APR-1991
                                                                                                                                                                                                                                                                                                                                           AAP70203
                                                                                                                                                                                                                                                                                                                                                                     AAP70203 standard; protein; 426
                                                                                          Cleavage-site
                                                                                                                                                             Region
                                                                                                                                                                                                                                 Homo sapiens
                                                   EP222491-A
                                                                                                                                    Region
                       20-MAY-1987
                                                                                                                                                                                         Modifled-site
                                                                                                                                                                                                                                                                                                                                                                                                                                          426 CS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 SLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 GLSTINQTRLDFHFS---SDRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 CS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 AASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRPTLNRPVSRAALRTALQHLH-------GVPQGALLEDNREQECEIISFAET 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLAFLLLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOIHRRGIDCOGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACEQCHETGASLVLLGKKKKKEEEAEGRKRDGEGAGVDEEKEQSHRPFLMLQARQSEEHP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACSQGHLT-LELVLEGQVAQSSVILGG------AAHRPFVAARVRVGGK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGSADAGEEAEDVGFPEEKSEVLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSALDIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XGTAXXRKTLRFEISKEGSDLSV----VERAEIWLFLKVPKANRTRTKVSIRLFQQQRRP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 AA;
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                          Location/Qualifiers 165..167
                                                                                                        /note="pro region" 311..326
                                                                             /note="proteolytic processing site"
                                                                                                                                                                           /note="potential N-linked glycosylation sites"
                                                                                                                                                /note="signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70; Mismatches 141;
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Pred. No. 1.2e-45;
                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                             spermatogenesis
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02-OCT-1986;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1986;
03-OCT-1985;
10-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 8A; 48pp; English.
425 CS
                                                                                                                                                                                                          245
                                 351 CS
                                                           365 SLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG
                                                                                                      291
                                                                                                                                         305
                                                                                                                                                                                                                                             204
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                                                                                                                                                                                                                                                                                                                                                                   105 GLSTINGTRLDFHFSSDRTAGDRE-VQQASLMFFVQLP-SNTTWT-LKVRVLVLGPH--- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAN70315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mason AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHEK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LLAFLLLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulating the climical condt. or reproductive physiology of
                                                                                          AASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACG
                                                                                                                                                                                                                                 QVAQSS----VILG------GA-----GA-----AHRPF--VAARVRVGGK 230
                                                                                                                             HRRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGS 364
                                                                                                                                                             HOIHRRGIDCOGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGI 290
                                                                                                                                                                                               EOCOESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHP 304
                                                                                                                                                                                                                                                                                                   ......NTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEG 203
                                                                                                                                                                                                                                                                                                                                      GTA----RKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKÝTIRLFQQQKHPQG 184
                                                                                                                                                                                                                                                                                                                                                                                                        KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAES 129
                                                                                                                                                                                                                                                                                                                                                                                                                                        QRPTLNRPVSRAALRTALQHLH------GVPQGALLEDNREQECEIISFAET 104
                                                                                                                                                                                                                                                                  SLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQPLLDQGKSSLDVRIAC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1987-137512/20
                                 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 AA;
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85US-0783910.
86US-0827710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.1%; Score 557; DB 8; Length 426; 31.5%; Pred. No. 1.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Also claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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RESULT 14 AAY92016

AAY92016 standard;

Protein; 426 AA

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Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological matching transforming growth factor facility.
                        Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                              This is the wild type human inhibin A beta subunit.

Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bloactivity.
                                                                                                                                                                                                                                                                                                                                                                                   New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g.
                                                                                                                                                                                                                                                                                                                                      Claim 283; Page 303; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                           hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weintraub BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200017350-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hairpin loop; infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human inhibin A beta subunit; CKGF; mutant; cystine knot growth factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Szkudlinski MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US19772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US05908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= beta_hairpin_loop_3
/note= "mutant optionally comprises one or substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "mutant optionally comprises one or more substitutions in these residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "optionally mutated to increase electrostatic interaction between beta hairpin structure as a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interaction between beta hairpin structure
a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a receptor"
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                      and in assisted reproduction
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY92018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY92018 standard; Protein; 426 AA
                                                                                                                                                                                                                                                                                                                                                                                             human activin A subunit; CKGF; mutant; cystine knot growth factor, hairoin loom: infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human activin A subunit.
                                              Misc-difference 420..426
                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                          Misc-difference 1..325
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        hairpin loop; infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 GTA----RKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQG
                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 CS 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 ORPTLNRPVSRAALRTALQHLH--------GVPQGALLEDNREQECEIISFAET 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 30.1%; Score 557; DB 21; Length 426; Local Similarity 31.5%; Pred. No. 1.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLAFLLLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLSTINGTRLDFHFSSDRTAGDRE-VQQASLMFFVQLP-SNTTWT-LKVRVLVLGPH--- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAES 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEG 203
                                                                                                                                                                           347..394
                                                                                                                                                                                                                                                                           /note- "optionally mutated to increase electrostatic
interaction between beta hairpin structure and
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                             /label= beta_hairpin_loop_3
/note= "mutant optionally comprises one or substitutions in these residues"
                                                                                                                                                                                                           /label- beta_hairpin_loop_1
/note- "mutant optionally comprises one or more
                /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure an
                                                                                                                                                              "optionally mutated to increase electrostatic
                                                                                                                             a receptor"
                                                                                                                                                                                             substitutions in these residues'
                                                                                                                                                                                                                                                           a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Mismatches 135;
                                                                                                                                              interaction between beta hairpin structure and
   receptor*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological activities of the CKGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200017360-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the wild type human activin A subunit.

Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bloactivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g. hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                130 GTA----RKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQG 184
365 SLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG
                       159 -----NTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEG
                                                                                                                                                                                                                                                                                                                                                                       105 GLSTINQTRLDFHFSSDRTAGDRE-VQQASLMFFVQLP-SNTTWT-LKVRVLVLGPH--- 158
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                                                                                                                                                                                                                                                                                                                                                                                                               70 KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LLAFILLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                 HRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGS 364
                                                                                                                       HQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGI 290
                                                                                                                                                                 EQCQESGASLVLLGKKKKKEEEGEGKKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHP
                                                                                                                                                                                                        QVAQSS----VILG-------GA-----AHRPF--VAARVRVGGK 230
                                                                                                                                                                                                                                              SLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDVRIAC 244
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B 5 351 CS 352 || 425 CS 426

Search completed: October 12, 2002, 02:06:05 Job time : 43 secs

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Title:
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e 1849; . No. 1 smatche	US/08482577B EERTRUD , HELGE , HELGE ROLF IS INA SEQUENCES ENCODING NOV: 49 49 59 50, MARKHELSTEIN, MURRAY, AND NTH STREET, N.W., G STREET N.W., G STREET ON Release #1.0, Version #1. ATA: US/08/482,577B 15 MATION: 36,335 4ATION: 37-5000 1810 NO: 2: FICS: BREAT P564-5010 FORMATION: 1-5000 1810 NO: 2: FICS: BREAT P564-5010 FORMATION: 1-5000 1810 NO: 2: FICS: BREAT P564-5010 FORMATION: 1-5000 1811 NO: 2: FICS: BREAT P564-5010 FORMATION: 1-5000 FORMATION: 1-5	US-09-184-933-12 US-08-455-550-12 US-08-65-844A-7 US-08-65-844A-7 US-08-55-596B-28 US-08-581-528A-18 US-08-581-528A-18 US-09-177-860A-28 US-09-145-060-24 PCT-US94-07762-18 PCT-US94-07762-18 PCT-US94-07799-18 US-08-481-377-22 US-08-491-835-20 US-09-153-733A-22 US-08-946-092A-20
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RESULT 2
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                                               REFERENCE/DOCKET NUMBER: PSTELECOMMUNICATION INFORMATION: 202/638-5000
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US U8/407/222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: DE P 44 23 190.3
                                                                                                           FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                              FILING DATE: 12-FEB-1992 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EPO 92102324.8
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B TITLE OF INVENTION: FAMILY
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                                                                                                                                                                     APPLICATION NUMBER: PCT/1
PTI.ING DATE: 12-FEB-1993
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE P
FILING DATE: 07-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 25-AUG-1999
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BECHTOLD, ROLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09218176 Patent No. 6171584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 352;
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
CLASSIFICATION:
                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: H TTEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: POHL, Jens
APPLICANT: PHILISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Roless
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                                                                                                                                            APPLICATION NUMBER: FILING DATE: Herew.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 LLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL 180
                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: $1
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                                                                                                                                                                                                                                                                                                                                                                                            Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                      E: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP 655 Fifteenth Street, N. W., G Street Lobby
                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                          US/09/218,176
PCT/EP96/03065
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FILING DATE: 12-JUL-PRIOR APPLICATION DATA:

12-JUL-1996

FILING DATE: APPLICATION NUMBER:

2-FEB-1993

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                                                                                                                                         Sequence 4, Application US/09054526B Patent No. 6197550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                       GENERAL INFORMATION:
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: BECHTOLD, ROLF
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: KITTS, MONICA Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: DE 195 11 FILING DATE: 27-MAR-1995 ATTORNEY/AGENT INFORMATION:
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                                                                                    APPLICANT:
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STRANDEDNESS: Sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 92 102 324. FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY, STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEPHAX: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                        PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS 120
                                                                       QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN
                                                                                                                                                                                                                   DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL
                                                                                                                                                                                                                                                       DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL 180
                                                                                         QGGSRWCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN 300
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APPLICANT: HOTTEN, GERTRUD
APPLICANT: HEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: BECHTOLD, ROLF
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-482-577B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-482-577B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08482577B Patent No. 5807713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202/030-40: (INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: 1.ENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
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NAME: KLESNER, SHARON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
300 NLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                     180 LLLGPEAQAACSOGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGID 239
                                                                                                                                             180 LPLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGID 239
                                                                                                                                                                                               121 G-RMASCMEVRQTREMFFVQFPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWVQ 179
                                                                                                                                                                                                                                        120 SDRTAGDREVQQASLMFFYQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQ 179
                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                        61 PTLNRPVSRAALRTALQHLHGVPQGALLE-DNREQECEIISFAETGLSTINQTRLDFHFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   1 MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                      CQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVL 299
                                                                                                                                                                                                                                                                                PILSRPVSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Mismatches
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; MOLECULE TYPE: US-09-218-176-4
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/482,577
FILING DATE: 7-JUN-1995
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                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                     APPLICATION NUMBER: DE 195 11 243.1 FILING DATE: 27-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA;
APPLICATION NUMBER: 1
FILING DATE: 01-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-FEB-
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ADDRESSEE: NIKAIDO, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE TITLE OF INVENTION: TGF- FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 655 Fifteenth Street, N. W., G Street Lobby, STREET: Suite 330
                                  TOPOLOGY:
                                              STRANDEDNESS:
                                                                                                                 TELEPHONE: 202/638-4810
                                                                                                                                                                                    REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                   NAME: KITTS, Monica Chin
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                                                               amino acid
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BECHTOLD, Rolf
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75.6%;

Score 1398;

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Length 352;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5929213
GENERAL INFORMATION:
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                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,662
FILING DATE: 28-APR-1997
                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lise A
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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             HYPOTHETICAL:
ANTI-SENSE:
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                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 07:
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                                                                   TOPOLOGY: 111
                                                                                                        TYPE: amino acids
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                                                                                                                         CENGTH:
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TYPE:
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                                                                                                                       350 amino acids
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                                                                                                                                                                                                                                                          07265/042WO1 (FD-3830)
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; ORIGINAL SOURCE: US-08-765-662-14
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GENERAL INFORMATION:
                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                     ANTI - SENSE:
                              MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 HLYHARLWLHV-LPT-LPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL---GWHTLTLP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 EVQQASLMFFVQLPSNTTWTLKVRVLVLGP----HNTNLTLATQYLLEVDASGWHQLPLG 183
FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                          TYPE: amino acids
                                                                          TOPOLOGY:
                                                                                           STRANDEDNESS:
                                                                                                                                                                                                        TELEFAX:
                                                                                                                            LENGTH:
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Best Local Similarity
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                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acid
                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: KLESNER, SHARON
                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA SEQUENCES ENCODING TITLE OF INVENTION: GROWTH/DIFFERENTIATION NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 HSAVESLLKANNPWPAST----SCCVPTARRPLSILYLDHNGNVVKTDVPDNVVEACGCS
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 STRANDEDNESS:
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                                                                                                                                              REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                              NAME: KLESNER, SHARON REGISTRATION NUMBER: 3
                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/482,577B
                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                           106 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            6: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM
655 FIFTEENTH STREET, N.W., G STREET LOBBY
SUITE 330
                                                                                          202/638-4810
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BECHTOLD, ROLF
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                  acid
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single
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43.3%; Pred. No. 1.1e-59;
ative 52; Mismatches 118; Indels 34; Gaps
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                                                                                                                                            P564-5010
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US-08-289-222E-28
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                                                                                                                                                                                         APPLICATION NUMBER: PCT/EP-
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,100
REFERENCE/DOCKET NUMBER: P
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                                                                                                                         INFORMATION FOR SEQ ID NO:
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              TOPOLOGY: 1: MOLECULE TYPE:
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US C
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
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                                               STRANDEDNESS
                                                                                                                      TELEPHONE: 202/638-4810
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Roles-
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FILING DATE: 07-JUL-1994
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                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 12-FEB
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BECHTOLD, ROLF
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25-AUG-1999
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100.0%; Pred. No. 7.3e-53;
tive 0; Mismatches 0;
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                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/482,577
PRIOR APPLICATION NUMBER: US 08/482,577
PILING DATE: 7-JUN-1995
PRIOR APPLICATION NUMBER: EP 92 102 324.8
PRIOR APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: DE P 44 23 190.3
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
NAME: KITTS, MONICO Chin
REGISTRATION NUMBER: 36.105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
                                                                      FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, Monica Chin
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hes 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/6
FILING DATE: 12-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: Herew!
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                           APPLICATION NUMBER: DE 195 11 243.1
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NEIDHARDT, Helge
BECHTOLD, Rolf
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IBM PC compatible
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100.0%; Pred. No. 7.3e-53;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                   TELEFAX: 202/638-4810 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
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            SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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TOPOLOGY: 11
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STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release
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                                                                                                                                      NAME: KITTS, MONICA CHIN REGISTRATION NUMBER: 36,105
                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 12-FE
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                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                      TELEPHONE:
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amino acid
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BECHTOLD, ROLF
                                                                      202/638-4810
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                                                   INFORMATION FOR SEQ ID NO: 43:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/958414
APPLICATION 08-0CT-1992
                 SEQUENCE CHARACTERISTICS LENGTH: 353 amino acid
                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1896
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
                                                                                                                                                                                                                                                           APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                     TELEPHONE: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 CCRQEFFVDFREIGWHDWIIQPEGYAMNFGIGQCPLHIAGMPGIAASFHTAVLNLLKANT 306
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FILING DATE: 16-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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amino acid
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                353 amino acids
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Patent No. 5665568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypept
TITLE OF INVENTION: Using such Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 138; Conservative
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                                                        APPLICATION NUMBER:
FILING DATE: 08-OCT-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,850
FILING DATE: 02-JUN-1995
                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
PRIOR APPLICATION DATA:
                                                                                                                               PRIOR APPLICATION DATA:
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               APPLICATION NUMBER: 07/7 FILING DATE: 12-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 RLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 LKRSGWHTEPLTEAIQALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 VDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVIL-----GGAAHRPFVAARV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 AGMPGIAASFHTAVLNLLKANTAAGTTGG--GSCCVPTARRPLSLLYYDRDSNIVKTDIP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 RVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 --GNQNLFVVQASLWLYLKL---LPYVLEKGSRRKVRVKVYFQEQGHGDRWNM-VEKRVD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 TAGDRE---VQQASLMFFVQLPSNTTWTL-----KVRVLVL---GPHNTNLTLATQYLLE 171
                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 HGVPQGALLEDNR------EQECETISFAETGLSTINQTRLDFHFSSDR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 CPACGGPTLELESQREL-----LLDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQHL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                94080
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                                                                               08-OCT-1992
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                                                                                                        07/958414
                                    07/744207
                                                                                                                                                                             08/197792
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                                                                                                                                                                     Sequence 43, Application US/08459214
Patent No. 5716810
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 43:
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LENGTH: 353 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
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FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
                                                                        APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
TITLE OF INVENTION: Using such Nucleic Acid
                  NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 VDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVIL-----GGAAHRPFVAARV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 --GNQNLFVVQASLWLYLKL---LPYVLEKGSRRKVRVKVYFQEQGHGDRWNM-VEKRVD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 TAGDRE--VQQASLMFFVQLPSNTTWTL-----KVRVLVL---GPHNTNLTLATQYLLE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 LKRSGWHTFPLTEAIQALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQA 226
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                                                                                                                                                                                                                                                                                                                           344 NMIVEECGCA 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 RVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGVPGSASSFHTAVVNQYRMR...-GLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVP 343
                                                                                                                                                                                                                                                                                                                                                                  DMVVEACGCS 352
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460 Point San Bruno Blvd
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03-OCT-1985
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37.3%; Pred. No. 4e-52;
ative 59; Mismatches 113; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
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STATE: California
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COMPUTER: I
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/958414 FILING DATE: 08-OCT-1992
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                                                                                                                 172 VDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVIL-----GGAAHRPEVAARV 225
                                                                                                                                                          113 -- GNQNLFVVQASLWLYLKL---LPYVLEKGSRRKVRVKVYFQEQGHGDRWNM-VEKRVD 166
                                                                                                                                                                                               123 TAGDRE--VOQASLMFFVQLPSNTTWTL-----KVRVLVL---GPHNTNLTLATQYLLE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 06/783910 FILING DATE: 03-OCT-1985
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227 RLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYL 286
                                    226 RVG-GKHQIHRRGIDCOGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGOCPLHI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                          80 HGVPQGALLEDNR-------EQECEIISFAETGLSTINQTRLDFHFSSDR 122
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                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity es 138; Conserv
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                                                                                                                                                                                                                                                                                                                     1 CTSCGG----FRRPEELGRVDGDFLEAVKRHILSRLQMRGRPNITHAVPKAAMVTALRKL 56
                                                                             LKRSGWHTFPLTEAIQALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQA 226
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Search completed: October 12, 2002, 02:10:48 Job time : 17.5 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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688.5
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1: pir1:*
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Gapop 10.0 , Gapext 0.5
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1849
1 MTSSLLLAFILLAPTTVATP......DSNIVKTDIPDMVVEACGCS 352
 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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pir2:*
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   JC2466
JC5366
S70580
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WFPGBA
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B24248
S50898
I40905
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inhibin beta-C cha activin beta C - m activin beta C - m activin beta C cha activin beta B sub betaB inhibin beta-B cha inhibin beta-B cha inhibin beta-B cha inhibin beta-A cha inhibin beta-B cha activin beta-B cha activin beta-B cha activin beta-B cha activin beta-B cha inhibin beta-B cha inhibin beta-B cha activin beta-B cha activin beta-B cha inhibin beta-B cha cha inhibin beta-B cha cha inhibin beta-B cha
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229.5	230.5	231	231	231.5	235	236.5	237	237	239.5	240	246.5	247	253	261	267
12.4	12.5	12.5	12.5	12.5	12.7	12.8	12.8	12.8	13.0	13.0	13.3	13.4	13.7	14.1	14.4
426	401	408	365	408	513	405	510	402	313	408	353	398	372	398	357
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JH0690	JH0689	S38343	T43286	вмни4	BMHU6	I50608	A54798	A45056	151284	S58791	I50607	JH0687	C39364	JH0688	A39364
bone morphogenetic	bone morphogenetic	bone morphogenetic	cet-1 procein - Ca	bone morphogenetic	bone morphogenetic	bone morphogenetic	Vg-1-related prote	osteogenic protein	bone morphogenetic	bone morphogenetic	bone morphogenetic	bone morphogenetic	GDF-1 embryonic gr	bone morphogenetic	GDF-1 embryonic gr

ALIGNMENTS

?	망	ν	Db	Qy	DЬ	Οу	Db	Qy	дb	Qy	Query M Best Lo Matches	C; Keyw F;1-18 F;19-2 F;237- F;110,	A; Cros	C; Genetics:	A;Cros	A; Mole	A; Title A; Refe	R; Hoet	C; Date	inhibir N;Alter	RESULT JC2466	
201	241	241	181	181	121	121	61	61	μ	۲	y Ma Loc hes	7 Dom 36/D 352/	s-re posi	tics	s-re rime	dues Sule	Cenco Cenco	cen,	29	naț	ъ	
ILKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352	QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN 300	QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN 300	PLGPEAQAACSQCHLTLELVLEGQVAQSSVILGGGAAHRPFVAARVRVGGKHQIHRRGIDC 240	PLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGIDC 240	DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL 180	DRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL 180	PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS 120	PTLNRPVSRAALRTALOHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS 120	MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60	MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60	Query Match 100.0%; Score 1849; DB 2; Length 352; Best Local Similarity 100.0%; Pred. No. 6.5e-159; Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	C;Reywords: glycoprotein C;Reywords: glycoprotein F;1-18/Domain: signal sequence #status predicted <sig> F;1-236/Domain: propeptide #status predicted <pro> F;237-352/Product: activin beta C #status predicted <mat> F;110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted</mat></pro></sig>	A;Ccoss-references: GDB:632884 A;Cross-references: GDB:632884 C;Map position: 2cen-2q13	ICS:	;Cross references: GB:X82540; NID:g669154; PIDN:CAA57890.1; PID:g669155		A;Title: Cloning of a new member of the TGF-beta family: A putative new activin betaC A;Reference number: JC2466; MUID:95128961	Schneider, C.; Pohl, J. . 206, 608-613, 1995	C;Sbecles: Homo sapiens (man) C;Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999	inhibin beta-C chain precursor - human N;Alternate names: activin beta C chain		

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A; Introns: 106/1
C; Superfamily: inhibin
                                                                                                                                                                                          C:Accession: $70580

R:Lau, A.L.: Nishimori, K.; Matzuk, M.M.

Biochim. Biophys. Acta 1307, 145-148, 1996

A:Title: Structural analysis of the mouse activin beta-C

A:Reference number: $70580; MUID:96283807
                                                                                                                                                                                                                                                                                                           activin beta C precursor - mouse C: Species: Mus musculus (house mouse)
                                                                                                    C; Genetics:
                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-352 <LAU>
                                                                                                                                                                                                                                                                                  C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
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                                                                                                                  A;Cross-references: EMBL:U40772
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Blochem. Biophys. Res. Commun. 231, 655-661, 1997
A;Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit A;Reference number: JC5366; MUID:97224404
A;Accession: JC5366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activin beta C - mouse
activin beta C - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
C:Accession: JC5366
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C:Superfamily: 1
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A; Residues: 1-352 <FAN>
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                                Query Match
              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment: Activin beta C and beta E form a distinct subset of related activins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              240 CQCGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 CQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGID 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 G-RMASGMEVROTREMEFVOEPHNATOTMNIRVLVLRPYDTNLTLTSOYVVOVNASGWYO 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SDRTAGDREVQQASLMEFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQ 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MASSLLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGID 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILSRPVSRGALKTALORLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.6%; Score 1398; DB 2; 76.2%; Pred. No. 3.1e-118;
            75.38;
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       Score 1392; DB 2;
Pred. No. 1.1e-117;
                       Length 352;
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F;1-253/Domain: signal sequence #status predicted <SIG>
F;254-367/Product: activin beta D chain #status predicted <MAT>
F;64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: embryo C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A;Title: Molecular cloning and functional analysis of a new activin beta subunit: a A;Reference number: JC4151; MUID:95275314
A;Accession: JC4151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: glycoprotein; mesoderm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: DDBJ:D49543; NID:g961512; PIDN:BAA08494.1; PID:g961513
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A; Residues: 1-367 <ODA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activin beta D chain precursor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
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289 GIAASFHTAVLNILKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEA 348
                                                                                                                                                                           186 PRWTGWQTFSLKSMLQTFFDGGNKSLQLELNCDGCQDVPVLANPNNSHQPFLVAQAKVHE 245
                                                           246 QSHHATKRSLNCDQNSNLCCRKDYYVDFKDIGWNDWIKPEGYQINYCMGLCPMHIAGAP
                                                                                                                230 K-HQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMP 288
                                                                                                                                                                                                                                   172 VDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGA--AHRPFVAARVRVGG
                                                                                                                                                                                                                                                                                           127 ITLNFQFTRDKEQ-SAHVLQAHLWLFFKANRTSQQNETIRLYLVQEAYSRRILISEKLIE
                                                                                                                                                                                                                                                                                                                                                 112 TRLDFHFSSDRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 HPVPRGAVANALRRLHLNKPRMEGLFGSNSWDSNTENTDTDQQSYEIISFAETEYTNENS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 RPVSRAALRTALOHLH-GVPQGALL-----EDNREQECETISFAETGLSTINQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 CQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTLLGALAASTQGLTKKS--QCPSCG-----VQDKEVMIELAKQQILQKLHLKERPNIT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.2%; Score 688.5; DB 2; 40.4%; Pred. No. 3.3e-54; tive 65; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 367;
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A;Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522
R;Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.
Biochem. Biophys. Res. Commun. 231, 655-661, 1997
A;Tille: Genes coding for mouse activin beta C and beta E are closely linked and exhibit A;Reference number: JC5366; MUID:97224404
A;Accession: JC5367
A;Molecule type: DNA
A;Residues: 1-350 CRA2>
A;Residues: 1-350 CRA2>
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C; Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 29-Oct-1999
C; Accession: JC5241; JC5367
C; Accession: JC5241; JC5367
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
R; Fang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.
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A;Title: Molecular cloning of the mouse activin beta E subunit gene.
A;Reference number: JC5241; MUID:97096313
A;Contents: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activin beta E chain precursor - mouse
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A; Residues: 1-350 <FAN>
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activin beta B subunit - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
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                                                                                                                                                                                                               350 S 350
                                                                                                                                                                                                                                                                                                                                  292 ASFHSAVFSLLKANNP -- WPAGSSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 TAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLE--VDASGWHQL 180
                                                                                                                                                                                                                                                                            352 S 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 TLPSSGLRSEDSGVVKLQLEFRPLDLNSTAAGLPRLLLDTAGQQRPFLELKIRANEPGAG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 PLWSHHLYHARL--WLHVPPSFPGTLYLRIFRCG--TTRCRGFRTFLAEHQTTSSGWHAL 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLGPEAQAACSQGHLTLELVLEGQVAQSS-----VILGGAA-HRPFVAARVRVG--GKH 231
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                                                                                                                                                                                                                                                                                                                                                                ASPHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RARRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153;
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R;Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; FIELUS, A.; TWOLL, A....
Dev. Biol. 157, 474-483, 1993
A;Title: Expression of activin mRNA during early development in Xenopus laevis.
A;Reference number: I51199; MUID:93273083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:S61773; NID:g386027; PIDN:AAB26863.1; PID:g386028 C;Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                                          R:Thompson, D.A.; Cronin, C.N.; Martin, F. Eur. J. Biochem. 226, 751-764, 1994
A:Title: Genomic cloning and sequence analyses
y DNase I footprinting.
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C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
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A; Residues: 1-408 < THO>
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                                                                                                                                                                              C; Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S50897; MUID:95112839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 DDVTASRVRLSFTIANE---GNQNLEVFQSNLWLYLKLPEVMDKSRRKIRIKVHFQDAFN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 GLSTINQTRLDFHFSSDRTAGDRE--VQQASLMFFVQLP---SNTTWTLKVRVLVLGPHN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 YDRDSNIYKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 YGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR---GLNPGTVNSCCIPTKLSTMSMLY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 32.9%; Score 607.5; DB Local Similarity 36.6%; Pred. No. 6.7e-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 ITHMVPRAAMVSALRKLHA---GRVREDGNLEIPDLDGHSLPPPGHSTENSAETITFAET 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 LNRPVSRAALRTALQHLHGVPOGALLED------NREQECEIISFAET 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LLLPLLLAGLARTCAPSPTPEPGCPSC-HPPMEPE-----MLEAVKRHILTLLHMQDRPN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LLLAFIL--LAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPT 62
                                    13 APTTVATPRA------GGQ---CPACGGPTLELESQREL------LLDLAKRSIL 52
29 SPTPPPLPAAPQPPPPPPGAPGGSQDTCTSCGG----FRRPEELGRVDGDFLEAVKRHIL 84
                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG---GSCCVPTARRPLSLLY 329
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                                                                                       145;
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                                                                                       Conservative
                                                                                                                                                                                                                                                   EMBL: U16240
                                                                                                           32.7%; Score 605; DB 2; Length 408; 36.6%; Pred. No. 1.3e-46;
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                                                                                           Mismatches 117; Indels
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C:Superfamily: inhibin C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone F:1-207bomain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                         R;Schmelzer, C.H.; Burton, L.B.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, Blochim. Biophys. Acta 1039, 135-141, 1990
A;Title: Purification and characterization of recombinant human activin B. A;Reference number: S10751; MUID:90304183
A;Accession: S10751
                                                                                                                                                                                                        A:Molecule type: protein
A:Residues: 293-294,'GX',297-302,'XX',305-307 <SCH>
C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respection beta-A and beta-B, respectively.
                                                                                                                             A:Cross-references: GDB:119347; OMIM:147390
                                                                                                          A; Map position:
                                                                                                                                                                            A; Gene: GDB: INHBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:M31632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Characterization and regulation of testicular inhibin beta-subunit mRNA. A; Reference number: A40156; MUID:89295443
A; Accession: A40156
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A; Residues: 55-407 < MA2>
A; Residues: 55-407 < MA2>
A; Cross references: GB: M13437; NID: g186416; PIDN: AAA59169.1; PID: g186417
R; Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
Mol. Endocrinol. 3, 939-948, 1989
Mol. Endocrinol. 3, 939-948, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827 R;Mason, A.J.; Niall, H.D.; Sceburg, P.H. Blochem. Biophys. Res. Commun. 135, 957-964, 1986 A;Title: Structure of two human ovarian inhibins. A;Reference number: A90123; MUID:86186863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Mason, A.J.; Berkemeier, L.M.; Schmelzer, C.H.; Schwall, R.H.
Mol. Endocrinol. 3, 1352-1358, 1989
A;Title: Activin B: precursor sequences, genomic structure and in vitro activities.
A;Reference number: A40150; MUID:90114200
A;Accession: A40150
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000

C:Accession: A40150: C24248; A40156; S10751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: mRNA
A:Residues: 22-46,'A',48-407 <FEN>
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A; Residues: 1-407 <M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 IGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 CRELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AQSSVIL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFRE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 RKVRVKVYGQEQGPGDRWAAVEKRVDLKRSGWHTFPLTEPIQALFSRGERRLSLDVQCDS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 CEIISFAETGLSTINOTRLDFHFSSDRTAGDRE--VOQASLMFFVQLPSNTTWTL---- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR----GLNPGTVNSC
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C; Superfamily:
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R:Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, Mol. Endocrinol. 1, 388-396, 1987
                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-7 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
Mol. Endocrinol. 3, 1914-1925, 1989
A;Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit
A;Reference number: A41398; MUID:90190649
A;Accession: B41398
                          A; Molecule type: mRNA
A; Residues: 133-411 <ESC>
                                                                                                              A;Reference number: A40905; MUID:90331931
A;Accession: C40905
                                                                                                                                                    A; Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis
                                                                                                                                                                                                                                                                                                                                                                     A:Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin A:Reference number: 153288; MUID:94307180
A:Accession: I53288
                                                                     A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R)Dykema, J.C.; Mayo, K.E.
Endocrinology 135, 702-711, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M32756; GB:M32757; NID:g204943; PIDN:AAA41438.1; PID:g554460 R;Dykema, J.C.; Mayo, K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-174 <FEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Apr-1992 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C:Accession: B41398; 153288; C40905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibin beta-B chain precursor - rat
N;Alternate names: inhibin/activin beta B-chain
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F:293/Product: inhibin beta-B chain #status predicted <MAT>
F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A:Residues: 1-349 <a href="https://doi.org/10.11/">https://doi.org/10.11/</a>
A:Residues: 1-349 <a href="https://doi.org/10.11/">https://doi.org/10.11/</a>
A:Cross-references: GB:X03267; NID:g2005; PIDN:CAA27021.1; PID:g2006
A:Cross-references: GB:X03267; NID:g2005; PIDN:CAA27021.1; PID:g2006
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptid of comment forms of inhibin have been isolated (A and B) that differ in the amino-terminal different inhibin is secreted by ovaries or testes and inhibits the secretion of follit c:Superfamily: inhibin for the secreted in the secreted of the comment of the secreted by ovaries or testes and inhibits the secretion of follit c:Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibin beta-B chain precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reywords: contraceptive; follitropin inhibitor; glycoprotein; gonad; 1-234/Domain: propeptide (fragment) #status predicted <PRO>; 235-349/Product: inhibin beta-B chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A01394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 AVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTSLCCRQQFFIDFRLIGWN 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 KLSSMSMLYFDDEYNIVKRDVPNMIVEECGCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                              140 LPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLEL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
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                                                           131 LEKGSRRKVRVKVYFQEPGHGDRWDVVEKRVDLKRSGWHTLPLTEAIQALFERGERRLNL 190
200 VLEGQVAQSSVIL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEF 252
                                                                                                                                                                            74
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                                                                                                                                                                                                                                                                                                                                                44 LDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQHLHGVPQGALLEDNR------ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFREIGWH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIISFAETGLSTINQTRLDFHFSSDRTAGDRE--VQQASLMFFVQ-----LPSNTTWTLK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLHLTQRPTLNRPVSRAALRTALQHLHGVPQGALLEDNR------EQEC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTPPPSPAAPPPPPPPPGAPGGSQDTCTSCGGGGGGFRRPEELGRVDGDFLEAVKRHILS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSCCVPT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKVYFQEQGHGDRWNVVEKKVDLKRSGWHTFPITEAIQALFERGERRLNLDVQCDSCQEL 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR----GLNPGPVNSCCIPT
                                                                                                                                                                                                                                  -----EQECEIISFAETGLSTINQTRLDFHFSSDRTAGDRE--VQQASLMFFVQ----- 139
                                                                                                                                                                                                                                                                                          LEAVKRHILNRLOMRGRPNITHAVPKAAMVTALRKLHA---GKVREDGRVEIPHLDGHAS 73
                                                                                                                                                                            PGADGQERYSETISFAETDGLASSRVRLYFFISNE---GNQNLFVVQASLWLYLKLLPYV 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%; Score 587; DB 1; 37.7%; Pred. No. 4.4e-45;
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5; Mismatches 127; Indels
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activin beta B - zebra fish
C/Species: Brachydanio rerio (zebra fish)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C/Accession: I50103
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I50103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-393 <WIT>
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R; Wittbrodt, J.; Rosa, F.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 349
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                                                                              212 L-----GGAAHRPFVAARV-RVGGKHQIHRRGIDCQGGS-RMCCRQEFFVDFREIGWHD 263
363 LSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 393
                     264 WIIQPEGYAMNECIGQCPLHIAGMPGIAASEHTAVLNLLKANTAAGTTGG--GSCCVPTA 321
                                                                                                                                                                  246
                                                                                                                                                                                                                                                  187 SYEPGGQNVHWPM-MEKRVELKRSGWHTFPVSEAIREMLAKGGRRQDLDIHCEGCEAANV
                                                                                                                                                                                                                                                                                      156 ----GPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVI
                                                                                                                                                                                                                                                                                                                                  130 FAESDDVTPSKSSLYFLISNE---GNQNLYVLQANLWLYFKLMPGTLEKGLRAKVTVRVH
                                                                                                                                                                                                                                                                                                                                                                          101 FAETGLSTINQTRLDFHESSDRTAGDRE--VQQASL-MFFVQLPSNTTWTLKVRVLVL--
                                                                                                                                                                                                                                                                                                                                                                                                                  73 MRERPNITHPIPKAAMVTALRKLHA---GKVREDGRVEIPNLDGHAAHNEVQEETSEIIS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LTQRPTLNRPVSRAALRTALQHLHGVPQGALLEDNR------EQECEIIS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 LSYTCLMACLLSVQCSSLGAETGSQESQCVSCGLGHQEDSGRMDTDFLEAVKRHILNRLQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                LPILVDPSDPSHRPFLVVRAQQADGKHRIRKRGLECDGNNGGLCCRQQFYIDFRLIGWND 305
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Inhibin beta-A chain precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Species: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C:Accession: A01393
R:Mason, A.J.: Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R. Nature 318, 659-663, 1985

A; Title: Complementary DNA sequences of ovarian follicular fluid inhibin show

precurs

RESULT 12

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A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-424 <RES>
                                                                                                                                                                   A:Molecule type: protein
A:Residues: 309-311,'X',313-318,'XX',321-325 <AL2>
R:Albano, R.M.; Groome, N.; Smith, J.C.
Development 117, 711-723, 1993
                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A60087; I48265; S31440
A;Cross-references: EMBL:x69619; MID:g50145; PIDN:CAA49325.1; PID:g50146 C;Superfamily! inhibin
                                                                                                             A;Title: Activins are expressed in preimplantation mouse embryos and in ES A;Reference number: I48243; MUID:93321614
A;Accession: I48265
                                                                                                                                                                                                                                                                A;Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia ce A;Reference number: A60087; MUID:92155098
A;Accession: A60087
                                                                                                                                                                                                                                                                                                                       R;Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack, J., Development 110, 435-443, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: activin A; mesoderm-inducing factor WEHI-MIF
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A; Residues: 1-424 <MAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 SFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEACGCS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVELEDDIGRRAEMNELMEQTSEIITFAEA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LLASCWIIVRSSPTPGSGGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 ORPTLNRPVSRAALRTALOHLH.....-GVPQGALLEDNREQECEIISFAET 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LLAFILLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 30.4%; Local Similarity 31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRRRGLECDGKVNICCKKOFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQCHETGASLVLLGKKKKKEEEAEGRKRDGEGAGVDEEKEQSHRPFLMLQARQSEEHPHR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQGHLT-LELVLEGQVAQSSVILGG------AAHRPFVAARVRVGGK--HQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 562; DB 1
Pred. No. le-42;
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A;Cross-references: GB:M13436; NID:g186414; PIDN:AAA59168.1; PID:g307069 R;Murata, M.; Eto, Y.; Shibai, H.; Sakai, M.; Muramatsu, M. Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438, 1988
                                                                                                                                                                                                     A;Cross-references: GB:X04447; NID:g33928; PIDN:CAA28041.1; PID:g33929 R;Mason, A.J.; Niall, H.D.; Seeburg, P.H. Biochem. Biophys. Res. Commun. 135, 957-964, 1986 A;Tille: Structure of two human overian inhibins.
                                                                                                                                                                                                                                                                                                                                                                                                             R:Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, FEBS Lett. 206, 329-334, 1986
A:Title: Human inhibin genes. Genomic characterisation and sequencing A;Reference number: A91366; MUID:87005283
A:Accession: B23556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Tanimoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukamizu, A.
DNA Seq. 2, 103-110, 1991
A;Title: Structure and sequence analysis of the human activin beta(A) subunit gene.
A;Reference number: S30488; MUID:92135888
A;Accession: S30488
                                                                                                    A; Molecule type: mRNA
A; Residues: 1-426 < MAS>
                                                                                                                                                            A;Reference number: A90123; MUID:86186863
A;Accession: B24248
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 311-426 <STE>
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A;Molecule type: DNA
A;Residues: 1-426 <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X57578; NID:g28351; PIDN:CAAA/0805.1; PID:g825621
A;Note: the authors translated the codon GAG for residue 53 as Gly and GAG for residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C:Accession: S30488; B23556; B24248; A30884; S33351; PN0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibin beta-A chain precursor [validated] - human N_iAlternate names: activin A_i activin AB chain A_i erythroid differentiation factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 ASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSILYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 RRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 QIHRRGIDCQGGSRMCCRQEFFYDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 CEQCQESGASLVLLGKKKKKEVDGDGKKKDGSDGGLEEEKEQSHRPFLMLQARQSEDHPH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 ------NTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 TGLSTINQTRLDFHFSSDRTAGDRE-VQQASLMFFVQLP-SNTTWT-LKVRVLVLGPH-- 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 KKRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAE 128
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A; Description: Nucleotide S6
A; Reference number: S33351
A; Accession: S33351
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
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A;Title: Purification of megakaryocyte differentiation activity from a human fibrous his A;Reference number: PN0010; MUID:91144591
A;Accession: PN0010
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A;Residues: 311-313,'X',315-320,'XX',323-328,'X',330-334 <FUJ>
C;Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respect
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A; Residues: 1-426 <MUR>
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A;Map position: 7p15-7p13
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 GLSTINQTRLDFHFSSDRTAGDRE-VQQASLMFFVQLP-SNTTWT-LKVRVLVLGPH--- 158
                                                               351
                                                                                                                                                                                                                                                                                                                                       245
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             425 CS 426
                                                                                                                      365 SLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG 424
                                                                                                                                                                        291 AASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACG 35.0
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                                                                                                                                                                                                                                                                             HQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGI 290
                                                                                                                                                                                                                                                                                                                                     EQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHP 304
                                                                                                                                                                                                                                                                                                                                                                                            QVAQSS----VILG------GA-----GA-----AHRPF--VAARVRVGGK 230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAES 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRPTLNRPVSRAALRTALQHLH....-GVPQGALLEDNREQECETISFAET 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------NTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEG 203
                                                                  CS 352
                                                                                                                                                                                                                               HRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGS 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.1%; Score 557; DB 1; 31.5%; Pred. No. 2.9e-42;
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N;Alternate names: activin; mesoderm inducing factor C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999 C;Accession: $50898; B25732; A60960; B61548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 258-425 <FOR>
A;Residues: 258-425 <FOR>
A;Cross-references: GB:M13274; NID:g163196; PIDN:AAA97415.1; PID:g163197
A;Note: part of this sequence, including the amino end of the mature protein, R;Chertov, O.Y.; Krasnosel'skii, A.L.; Bogdanov, M.E.; Hoperskaya, O.A.
Biomed. Sci. 1, 499-506, 1990
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A;Title: Cloning and sequence analysis of cDNA species coding for the two subunits of A;Reference number: A94097; MUID:86205842
A;Accession: B25732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; homodimer; hormone F;1-28/Domain; signal sequence *status predicted <SIG>F;29-309/Domain; propeptide *status predicted <PRO>F;310-425/Product; beta-A inhibin/activin *status experimental <MAT>F;165/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M. Mol. Cell. Endocrinol. 44, 55-60, 1986
A;Title: Isolation of bovine follicular fluid inhibin of about 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Mesoderm-inducing factor from bovine amniotic fluid: purification A;Reference number: A60960; MUID:92126853 A;Accession: A60960
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A;Accession: $50898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 310-313 <FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A61548; MUID:86136989
A; Accession: B61548
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245 EQCQETGASLVLLGKKKKKEEEGEGKKRDGEGGAGGDEEKEQSHRPFLMLQARQSEDHPH
                                                                                                                                                                                       159 -----NTNLTLATQYLLEVDASGWIQLPLGPEAQAACSQGHLTLELVLEG
                                                                                                                             185 SLDAGEEAEEVGLKGEKSEMLISEKVVDARKSTWHIFPVSSCIQRLLDQGKSSLDIRIAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLK 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLAFILLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                                                                                                                                                                                       GTA----RKTLHFEISKEGSDLSVVERAEIWLFLKVPKANRTRSKVTIRLFQQQKHLQG
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Pred. No. 3.2
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                                                                   -GGA-----AHRPF--VAARVRVGGKH 231
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ON protein . protein search, using sw model
                                                                                GenCore version 5.1.3 copyright (c) 1993 - 2002 Compugen Ltd.
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October 11, 2002, 22:35:53; Search time 13.5 Seconds (without alignments) 1009.576 Million cell updates/sec

Title: . Perfect score: US-09-684-383-2 1849

1 MTSSLLLAFLLLAPTTVATP......DSNIVKTDIPDMVVEACGCS 352

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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BMP4_DAMDA	BM8A_MOUSE	DVR1_BRARE	BMPA_XENLA	BMP2_CHICK	GDFB_RAT	GDF1_HUMAN	GDF8_CHICK	GDF8_RAT	GDF8_MELGA	GDF8_PAPHA	BMPB_XENLA	
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	INLIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUTTARY HORMONE SECRETION, GENORADAL HORMONE SECRETION, GENORADAL HORMONE SECRETION, GENORED TO AN ATURATION, IENTERRENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBURIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF ACTIVINS. -1. SUBURIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH ALPHA AND BETA SUBURITS, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBURIT. ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBURITS ONLY (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Liver; MEDLINE-95126961; PubMed-7826378; Hoetten G., Neidhardt H., Schneider C., Pohl J.; Hoetten G., Neidhardt H., Schneider C., Pohl J.; Rottivin beta C chain."; Blochem. Biophys. Res. Commun. 206:608-613(1995). [2] TISSUE SPECIFICITY. MEDLINE-98089987; PubMed-9428386; MEDLINE-98089987; PubMed-9428386; Thomas T.Z., Chapman S.M., Hong W., Gurusingfhe C., Mellor S.L., Fletcher R., Pedersen J., Risbridger G.P.; "Inhibins, activins, and follistatins: expression of mRNAs and cellular localization in tissues from men with benign prostatic hyperplasia."; Prostate 34:34-43(1998). ACTIVINS INHIBIT AND ACTIVATE, -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, -1- FUNCTION: TABLES AND ACTIVINS INHIBIT AND ACTIVATE,	HUMAN IHBC_HUMAN STANDARD; PRT; 352 AA. P55103; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Inhibin beta C chain precursor (Activin beta-C chain). INHBC. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

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                           SEQUENCE FROM N.A.
STRAIN-129; TISSUE-Liver;
                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                  P55104; Q61452;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
         MEDLINE=96435913; PubMed=8838799; Schmitt J., Hoetten G., Jenkins N
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PROSITE; PROAPER
                                                                                                                                                                                     HBC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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InterPro: IPR001318; Inhibin_b
InterPro: IPR001839; TGF-beta.
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                                                                                                                                                                                                                                                                                      QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN
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                                                                                                                                                                                                                                                                                                                                                                                                                              PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                           PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTSSLLLAFILLAFTTVATPRAGGOCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352;
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Schrewe H.;
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        Hoetten G., Jenkins N.A.,
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ilarity 100.0%;
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                                                                                                                            precursor
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Inhibin_betaC.
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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

496476AD82562D3E CRC64;
                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                    PRT;
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Pred. No. 3.6e-161;
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BY SIMILARITY.
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PRINTS; PRO0672; INHIBINBC.
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                 InterPro: IPR002400; GF_cysknot.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fang J., Wang S.Q., Smiley E., Bonadio J.;

"Genes coding for mouse activin beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues.";

Biochem. Biophys. Res. Commun. 231:655-661(1997).

-!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

RESPECTIVELY, THE SECRETION OF FOLLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

ERYTHROID DIFFERENTIATION, GERM CELL DEVELOPMENT AND MATURATION,

ERYTHROID DIFFERENTIATION, GERM CELL SURVIVAL,

EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lau A.L., Nishimori K., Matzuk M.M.; "Structural analysis of the mouse activin beta C gene."; Biochim. Biophys. Acta 1307:145-148(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97224404; PubMed=9070865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96283807; PubMed=8679697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT LIVER. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BO INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY STATIA DETAY).
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BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
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N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
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-> G (IN REF. 1)
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CRC64;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAT 3
                                                                                                                                                                                                                                                                                                                        "Rat activin beta C and beta E: sequence and expression.";

Submitted (APR-1999) to the EMBL/GenBank/DIBJ databases.

11- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

ERYTHROID DIPFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,

EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THBC_RAT STANDARD; PRT; 351 AA. 09WUK5; 09WUK5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-DCT-2001 (Rel. 40, Last annotation update) 10hibin beta C chain precursor (Activin beta-C chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rossmanith W., Peter B., Schulte-Hermann R.;
Rat activin beta C and beta E: sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                       ACTIVINS.
SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
                                                                                                                                                                                  SIMILARITY).
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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PRINTS; PRO0672; INHIBINBC.
PRODOM; PD000357; TGF-beta; 1.
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InterPro; IPR001318; Inhibin_betac.
InterPro; IPR001839; TGF-beta.
Pfam: PF00019; TGF-beta; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00204; TGFB; 1
                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                   SEQUENCE FROM N.A.
TISSUE-Rhabdomyosarcoma;
                                                                                                                                                                                                                                                                                                                                                                       IHBE_HUMAN
P58166;
                      Submitted (MAR-2001) to
                                            Strausberg R.;
                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                     Inhibin beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 LLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 LLGPEAQAACSOGHLTLELVPESQLAHSSLILDGVSHRPFVAAQVRVEGKHRVRRRGINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESORELLLDLAKRSILDKLHLTQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRTAGDREVOQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASSILLALLEITLATVVNLKTDGPCPACWGATFDLESHREILLDLAKKSILDKIHLSQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLGPEAQAACSQGHLTLELYLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILSRPVSREALKTALRRLRGTRAETLLEHDQRQEYEIISFADTGLSNINQTRLEFHF-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTLNRPVSRAALRTALQHLHGVPQGALLEDNREQECEIISFAETGLSTINQTRLDFHFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKANTDAGTARRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGLSRMCCRQEFFYDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRTTGGVEVLQTRFMFFMQLPPNTTQTMNIRVLVLRPYDTNLTLTSQYMLQVDASGWYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor;
                                                                                                                                                                                                                                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
a E chain precursor (Activin beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
  INHIBINS
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                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGF_BETA_1; 1.
                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.6%;
75.6%;
  AND
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                        the
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  e EMBL/GenBank/DDBJ
ACTIVINS INHIBIT A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
6B219BF6C3E180A1 CRC64;
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                                                                                                                                                                         Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
TIBIT
                                                                                                                                                                                                                                                                                                                                                                                                  350
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                                                                                                                                                                                                  Vertebrata;
                                                                                                                                                                                                                                                                          beta-E chain).
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                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Matches
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DISULFID
DISULFID
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0669; INHIBINA.
PRINTS; PRO0672; INHIBINBC.
PRODOM; PD0000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
Pfam; PF00019; TGF-beta; 1.
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184
                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                     69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, SUBURIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMERIC OR HETERODIMERTC THROUGH ASSOCIATION WITH ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT. ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
                                                                                                                                                                                                                                                                                                                                                                                                     RAALRTALOHLHGVPQGALLEDNREQECEIISFAE-TGLSTINOTRLDFHFSSDRTAGDR 127
                                         HTAVLNLLKANT - - AAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
                                                                                      RRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASF
                                                                                                                                                                               SSGLRGEKSGVLKLQLDCRPLEGNSTVTGQPRRLLDTAGHQQPFLELKIRANEPGAGRAR
                                                                                                                                                                                                                        PEAQAACSQGHLTLEL---VLEGQ----VAQSSVILGGAAH-RPFVAARVRVG--GKHQIH
                                                                                                                                                                                                                                                                      HLYHARLWLHV-LPT-LPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL---GWHTLTLP 174
                                                                                                                                                                                                                                                                                                                 EVQQASLMFFVQLPSNTTWTLKVRVLVLGP----HNTNLTLATQYLLEVDASGWHQLPLG 183
                                                                                                                                                                                                                                                                                                                                                              QAALTRALRRLQ---PGSVAPGNGE---EVISFATVTDSTSAYSSLLTFHLSTPRS---H
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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actor; Hormone; Glycoprotein; Signal.
1 19 POTENTIAL.
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237
240
247
276
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314
198
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 664; DB 1; Pred. No. 4.3e-53;
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N-LINKED (GLCNAC. . .) (PO
; A49C1495677E3E6F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 350;
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                                           352
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RESULT 5
                                                                                    PROSITE;
Growth fa
SIGNAL
DISULFID DISULFID DISULFID
                                                  PROPEP
CHAIN
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Fang J., Wang S.O., Smiley E., Bonadio J.;

"Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues.";

Biochem. Blophys. Res. Commun. 231:655-661(1997).

-i- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GENTHROID DIFFERENTIATION, INSULIN SECRETION, NEARLY CELL SURVIVAL, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NEARLY CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                   PRINTS; PRO0438; GFCYSKNOT.
PRINTS; PR00672; INHIBINGC.
PRODOM; PD000357; TGF-beta;
SMART; SM00204; TGFB: 1.
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          InterPro; IPR002400; GF_cysknot.
InterPro; IPR001318; Inhlbin_betaC.
InterPro; IPR001839; TGF-beta.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHBE_MOUSE 008717;
                                                                                                                                                                                                                                                                                                  EMBL; U96386;
HSSP; P12643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fang J., Yin W., Smiley E., Wang S.O., Bonadio J.; "Molecular cloning of the mouse activin beta E subunit gene."; Biochem. Biophys. Res. Commun. 228:669-674(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                MGD; MGI:109269; Inhbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97224404; PubMed=9070865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97096313; PubMed-8941337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Inhibin beta E chain precursor (Activi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNHBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVINS.
SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT. ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY SIMILARITY).
SIMILARITY).
DEVULOPMENTAL STAGE: FIRST EXPRESSION IN EMBRYONIC LIVER IS DETECTED AT DAY E17.5.
                                                                                                     factor;
                                                                                                                     PS00250; TGF_BETA_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mouse).
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3BMP.
                                                                                                  Hormone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Chordata;
; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor (Activin beta-E chain)
                                                                                      Glycoprotein; Signal.
POTENTIAL.
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INHIBIN BETA E CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     088959; 09R285;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta E chain precursor (Activin beta-E chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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ROSSMANITH W., Peter B., Schulte-Hermann R.;

RAI activin beta C and beta E: sequence and expression.;

Submitted (APR-199) to the EMBL/GenBank/DDBJ databases.

-I- PUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

ERYTHROID DIFFERENTIATION, INSULIN SECRETION, DEPENDING ON THEIR
EXHBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY: TISSUE-Liver, and Lung:
MEDLINE-20290891; PubMed-10828834;
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                          O'Bryan M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                      STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        MOL.
                                                                                                                                                                                                                                                                        Kretser D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLGPEAQAACSQGHLTLELVLEGQVAQSS-----VILGGAA-HRPFVAARVRVG--GKH 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLE--VDASGWHQL 180
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                                                                                                                                                                                                                                      and regulation of the rat activin betaE subunit.";
Endocrinol. 24:409-418(2000).
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Pred. No. 1.2e-51;
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INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . . ) (PO
                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0438; GFCYSKNOT PRINTS; PRO0672; INHIBINBC
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HSSP; P12643; 3BMP
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SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT. ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVSRAALRTALQHLHGVPQGALLEDNREQECEIISFA---ETGLSTINQTRLDFHFSSDR 122
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                                                                                                     RARRRTPTCESETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA
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RESULT 7
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Pfam; PF00688; TGFb_propeptide; 1
Pfam; PF006438; GFCYSKNOT.
PRINTS; PR00671; INHIBLUBB
PRODOM; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
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                                                                                                                  Growth factor; SIGNAL
                                                                                                                                                                                                                                                       InterPro; IPR002400; GF_cysknot.
InterPro; IPR000381; Inhibin_betaB.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                         EMBL; U16241; AAB60628.1; -.
EMBL; U16240; AAB60628.1; JOINED.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson D.A., Cronin C.N., Martin F., "Genomic cloning and sequence analyses of the bovine alpha-, beta and beta B-inhibin/activin genes. Identification of transcription factor AP-2-binding sites in the 5'-flanking regions by DNase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta B chain precursor (Activin beta-B chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IHBB_BOVIN
P42917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cootprinting."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF BETA-A.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. BIOGHEM. 226:751-764 (1994).

J. BIOGHEM. 226:751-764 (1994).

FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELLY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. INHIBINS/ACTIVING ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, RERVE CELL SURVIVAL, EMPRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVINS.
                                                                                                                                             PS00250; TGF_BETA_1; 1.
    294
294
297
304
333
337
372
   Hormone;
1 28
9 293
4 408
7 305
4 373
3 405
7 407
2 372
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                                                                                                                               Glycoprotein;
              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 INTERCHAIN
                                                                             INHIBIN BETA B CHAIN
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(BY
SIMILARITY).
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MEDLINE=86186863; PubMed=3754442;
Mason A.J., Niall H.D., Seeburg P.H.;
Mason A.J., Niall H.D., Seeburg P.H.;
"Structure of two human ovarian inhibins.";
Biochem. Biophys. Res. Commun. 135.957-964(1986).
-i- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta B chain precursor (Activin beta-B
                                                                                                                           SEQUENCE OF 55-407 FROM N.A.
                                                                                                                                                                                                                       MEDLINE-89295443;
                                                                                                                                                                                                                                                                                    "Activin B: precursor sequences, genomic activities.";
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; vertebrata; i
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                         Mol. Endocrinol. 3:939-948(1989).
                                                                                                                                                                                      "Characterization and regulation of testicular inhibin beta-subunit
                                                                                                                                                                                                                                        SEQUENCE OF 22-407 FROM N.A
                                                                                                                                                                                                                                                                   Mol. Endocrinol. 3:1352-1358(1989)
                                                                                                                                                                                                                                                                                                                    Mason A.J.,
                                                                                                                                                                                                                                                                                                                                MEDLINE=90114200; PubMed=2575216;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHBB_HUMAN
P09529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
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                                                                                                                                                                                                        Z.M., Bardin C.W., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEIISFAETGLSTINOTRLDFHFSSDRTAGDRE--VQQASLMFFVQLPSNTTWTL----- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APTTVATPRA-----GGQ---CPACGGPTLELESQREL-----LLDLAKRSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR---GLNPGTVNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGWHDWIIQPEGYAMNECIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQSSVIL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKVRVKVYGQEQGPGDRWAAVEKRVDLKRSGWHTFPLTEPIQALFSRGERRLSLDVQCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KVRVLVLGPHN--TNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRLQMRGRPNITHAVPKAAMVTALRKLHA----GKVREDGRVEIPHLDGHASPGADGQERV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKLHLTQRPTLNRPVSRAALRTALQHLHGVPQGALLEDNR-------EQE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTPPPLPAAPQPPPPPPGAPGGSQDTCTSCGG----FRRPEELGRVDGDFLEAVKRHIL 84
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408 AA;
                                                                                                                                                                                                                                                                                                                    Berkemeier L.M.,
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                                                                                                                                                                                                                      PubMed-2739657;
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44897 MW;
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36.6%;
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                                                                                                                                                                                                                                                                                                               Schmelzer C.H.,
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                                                                                                                                                                                                                                                                                                             Schwall R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain)
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                                                                                                                                                                                                                                                                                Matches
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EMBL; M31668; AAA59451.1; JOINED.
EMBL; M31682; AAA59170.1; -.
EMBL; M13437; AAA59169.1; -.
PIR; C24248; C24248.
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00019: TGF-beta; 1.
Pfam; PF00688: TGFb_propeptide; 1.
PF1NTS; PR00438: GFCYSKNOT.
PRINTS; PR00671: INHTBINBB.
ProDom; PD000357: TGF-beta; 1.
SMART; SM00204: TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MIM; 147390; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000381; Inhibin_b
Interpro; IPR001839; TGF-beta.
Interpro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002400; GF_cysknot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00250; TGF_BETA_1; 1
                                                                                                                                                                                                                                                                                                                                                            CONFLICT
   206
                                 196
                                                                                             142
                                                                149
                                                                                                                          97
                                                                                                                                                          85
                                                                                                                                                                                   29
                                                                                                                                                                                                                                                  13 APTTVATPRA------GGQ---CPACGGPTLELESQREL-----LLDLAKRSILD 53
                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBIN A IS A DIMER OF ALPHA AND BETA-A. INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
                                                                                                                                                                                                                                                                                   145;
                                                                                                                                                                                                                      SPTPPPTPAAPPPPPPPGSPGGSQDTCTSCGG----FRRPEELGRVDGDFLEAVKRHILS 84
   AQSSVIL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFRE
                                  KVRVKVYFQEQGHGDRWNM-VEKRVDLKRSGWHTFPLTEAIQALFERGERRLNLDVQCDS
                                                                                             EIISFAETDGLASSRVRLYFFISNE---GNQNLFVVQASLWLYLKL---LPYVLEKGSRR 195
                                                                                                                         EIISFAETGLSTINOTRLDFHFSSDRTAGDRE--VQQASLMFFVQLPSNTTWTL----- 148
                                                                                                                                                        RLQMRGRPNITHAVPKAAMVTALRKLHA---GKVREDGRVEIPHLDGHASPGADGQERVS 141
                                                               KVRVLVL---GPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQV 205
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                              407
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone;
                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                            404
406
371
                                                                                                                                                                                                                                                                                                                                              45121 MW;
                                                                                                                                                                                                                                                                                             32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTE
S -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                              Score 599.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INHIBIN BETA B CHAIN.
                                                                                                                                                                                                                                                                                                                                               90316C83597BA6B4 CRC64;
                                                                                                                                                                                                                                                                                   Mismatches 118;
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                                                                                                                                                                                                                                                                                                  3.9e-47
                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                          . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                Length 407;
                                                                                                                                                                                                                                                                                   73; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P27093; 073796;
01-AUG-1992 (Rel. 23, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-91029482; PubMed-2225063; Mitrani E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Bril A.; Mctivin can induce the formation of axial structures and is expressed in the hypoblast of the chick."; Cell 63:495-501(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WHITE LEGHORN; TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klinger H., Halaschek-Wiener J., Wohlrab B.K., Kuchler K
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibin beta B chain precursor (Activin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Follicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHBB_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 311-381 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hecht D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 CQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRL
                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 CIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 IGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR---GLNPGTVNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
RESPECTIVING ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                    SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
INHIBIN B IS A DIMER OF BETA-A.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A DIMER OF BETA-B.
L; Z71594; CAA96248.1; -.
L; AF055478; AAC14187.1; -.
L; M61166; AAA48568.1; -.
L; M57408; AAA03079.1; -.
P; P18075; 1BMP.
                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSC
                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ryan I.M., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.A.;
                                                                                                                                                     Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain).
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                                                                                                                                                                                           restrictions on
                                                                                                                                                            for commerc
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THBB
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 136;
                                                                                                                                                                          InterPro: IPR002400; GF_cysknot.
InterPro: IPR001839; TGF-beta.
InterPro: IPR00111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00588; TGFb_propeptide; 1.
PRINTS: PR00438; GFCYSKNOT.
PRODOM: PD000337; TGF-beta; 1.
SMART: SM00204; TGFB; 1.
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
       Mason A.J., Hayflick J.S.,
                              MEDLINE-86092207; PubMed-2417121;
                                                                           SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                IHBB_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 RRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 WIIOPEGYAMNFCIGOCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSCCVPTA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 VLPIYVDPGEESHRPFLVVQARLADNKHRIRKRGLECDGRTNLCCRQQFYIDFRLIGWND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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                                                    SSUE-Ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LAALLACGLLLLGAAATPTPPPAGSSPQDTCTSCGFRRPEEPGKVDGDFLEAVKRHILSR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTSSLLLAFILLAPTTVATPRAGGQ-----CPACGGPTLELESQRE-LLLDLAKRSILDK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIIAPSGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR---GLNPGTVNSCCIPTK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVYFQDPDTSNKWNVVEKKVDLKRSGWHTFPMTEAIQALFERGERRLNLDVQCEGCEEYS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVLVLGPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQMRDRPNITHAVPKAAMVTALRKLHA---GKVREDGRVEIPSLDGQASAGPPAHDPVSE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISFAETGLSTINGTRLDFHFSSDRTAGDRE--VQQASLMFFVQ-----LPSNTTWTLKV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IL-----GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISFAETDDLASSRVRLYFFISNE---GNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                      follicular fluid;
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  Ling N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 598; DB 1;
Pred. No. 5.1e-47;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBIN BETA B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 138; Indels
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  Esch F.,
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                                                                                                                                              Suidae; Sus
Ueno N.,
                                                                                                                                                                 Euteleostomi;
Ying
S. -Y.
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InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb_propeptide;
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                          SEQUENCE
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140 LPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLEL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00204; TGFB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N., Ariizumi T., Yashiro T., Sugino K., Titani K., Sugino H.;

"Isolation and characterization of native activin B.";

J. Biol. Chem. 267:16385-16389(1992)

'I' FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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"Complementary DNA sequences of ovarian follicular fluid inhibin show precursor structure and homology with transforming growth factor-beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE * 92355604;
                                     74 PGADGQERVSEIISFAETDGLASSRVRLYFFISNE---GNONLFVVQASLWLYLKLLPYV 130
                                                                                      93
                                                                                                              17 LEAVKRHILNRLOMRGRPNITHAVPKAAMVTALRKLHA---GKVREDGRVEIPHLDGHAS
                                                                                                                                                    44 LDLAKRSILDKLHLTORPTLNRPVSRAALRTALQHLHGVPQGALLEDNR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                           -----EQECEIISFAETGLSTINQTRLDFHFSSDRTAGDRE--VQQASLMFFVQ----- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor; Hormone;
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                          349
                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                      39354 MW;
                                                                                                                                                                                                            31.7%; Score 587; 37.7%; Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein.
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
(POTENTIAL).
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                                                                                                                                                                                             Mismatches 109;
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P03970;
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92355604; PUNMED-1644823;

NAKABMURA T., ASASAHMB M., EtO Y., Takio K., Uchiyama H., Moriya N.,

Ariizumi T., Yashiro T., Sugino K., Titani K., Sugino H.;

"Isolation and characterization of native activin B.";

J. Biol. Chem. 267:16385-16389(1992).

-I. FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

FUNCTION: THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION OF SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, ERRYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, ERBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-Follicular fluid;
MEDLINE-86092207; PubMed-2417121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y., Guillemin R., Niall H., Seeburg P.H.; Complementary DNA sequences of ovarian follicular fluid inhibin show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
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                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Follicular fluid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 318:659-663(1985).
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INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration when the Swiss Institute of Bioinformatics and the EMBL outstation burspean Bioinformatics Institute. There are no restrictions on its burspean Bioinformatics Institute. There are no restrictions on its burspean bioinformatics institute.
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A01393; WFPGBA.
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SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
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InterPro: IPR001839; TGF-beta.
InterPro: IPR001111; TGFb_N.
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P18331;
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                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
SEQUENCE FROM N.A. MEDLINE-91042598;
                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                     NCBI_TaxID-10116;
                                                                             Rattus norvegicus (Rat)
                                                                                                 L6-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta A chain precursor (Activin beta-A chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                          293 SFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
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                                                                                                                                                                                                                                                                                                                                          EQCHETGASLVLLGKKKKKEEEAEGRKRDGEGAGVDEEKEQSHRPFLMLQARQSEEHPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      -----PHNTNLTLATQYLLEVDASGWHQLPLGPEAQ------AAC 190
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                                                                                                                                                                      STANDARD;
                                                                                                                                          16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308
424
320
389
421
423
388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47476 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 562; DB 1;
Pred. No. 1.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (F
436BC62226FDAF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INHIBIN BETA A CHAIN.
                                                  Craniata; Ver
Sciurognathi;
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                       424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                   Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                         Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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PubMed-3153478;

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Best Local
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DISULFID
DISULFID
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00019; TGF-beta; 1.
Pfam: PF00688; TGFb_propeptide; 1.
PRINTS: PR00438; GFCYSKNOT.
PRINTS: PR00670; INHJBINBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
153 --LVLGPHNTNLTL---ATQYLLE---VDA--SGWHQLPLGPEAQAACSQGHLTLELVLE 202
                                                                          129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00204
                                                                                                                               104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002400; GF_cysknot.
InterPro; IPR000491; Inhibin_betaA.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M37482; AAA41436.1; -.
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                                                                                                                                                             69 KKRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAE 128
                                                                                                                                                                                                                  58 TORPTLNRPVSRAALRTALOHLH-------GVPQGALLEDNREQECEIISFAE 193
                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                              6 LLAFLLLAPTTVATPRAGG-----QCPACGGPTLELE---SQRELLLDLAKRSILDKLHL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLEMENTARY GLAND.

ENDOGRINGI. 1:561-568(1987).

ENDOGRINGI. 1:561-568(1987).

FUNCTION: INHIBLYS AND ACTIVINS INHIBIT AND ACTIVATE,

FUNCTION: INHIBLYS AND ACTIVINS OF FOLLITROPIN BY THE PITUITARY GLAND.

RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITULTARY HORMONE SECRETION,

FUNCTIONS SUCH AS
                                                                                                           TGLSTINGTRLDFHFSSDRTAGDRE-VQQASLMFFVQLPSNTTWTLKVRV------ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INHIBIN A IS A DIMER OF ALPHA AND BETA-A. INHIBIN B IS A DIMER OF ALPHA AND BETA-B. ACTIVIN A IS A HOMODIMER OF BETA-A. ACTIVIN B IS A HOMODIMER OF BETA-B. ACTIVIN B IS A HOMODIMER OF BETA-B. ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                       SGTA----RKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQ 183
                                                                                                                                                                                                                                                                         LLASCWIIVRSSPTPGSEGHGAAPDCPSCALATLPKDGPNSQPE-MVEAVKKHILNMLHL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B40056; B40056.
; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r; Hormone; Glycoprotein; Signal.

1 20 POTENTIAL.

21 308
309 424 INHIBIN BETA A CHA
309 424 BY SIMILARITY.
319 389 BY SIMILARITY.
348 421 BY SIMILARITY.
352 423 BY SIMILARITY.
352 423 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGFB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         30.3%;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                        Score 561; Ds 1,
No. 1.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INHIBIN BETA A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B2DAF7917FA50984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 424;
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RESULT 13
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                                                                                          EMBL; D50326; BAA08862.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                           entities requires a license agreement (See http://www.isb·slb.ch/announce/
                                                                                                                                                                                                           This SNISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Vet. Med. Sci. 57:469-473(1995).

-i- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                    <del>:</del>
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang K., Matsuyama S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Perissodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of cDNA for equine ovarian inhibin/activin beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshida S., Yamanouchi K., Hasegawa T., Ikeda A., Suzuki M.,
Chang K., Matsuyama S., Nishihara M., Takahashi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96031670; PubMed-7548399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibin beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 ASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 CEQCQESGASLVLLGKKKKKEVDGDGKKKDGSDGGLEEEKEQSHRPFLMLQARQSEDHPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                      ACTIVINS.

SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A HOMODIMER OF BETA-B.

ACTIVIN B IS A HOMODIMER OF BETA-B.

ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQVAQSS----VILG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A chain precursor (Activin beta-A chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata: Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                            BONDS
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Pfam; PF00019;

TGF-beta;

InterPro;

InterPro; InterPro;

IPR002400; GF_cysknot. IPR000491; Inhibin_betaA. IPR001839; TGF-beta. IPR001111; TGFb_N.

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 RRRRROCCOGGETTTAL
                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                            IHBA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00688; TGFb_propeptide; PRINTS; PR00438; GFC7SNROT. PRINTS; PR00670; INHIBINBA. ProDom; PD000357; TGF-beta; 1. SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                THBA_MOUSE STANDARD; PRT; 424 AA. Q04998; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
Albano P.M., Groome N., "Activins are expressed
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                             MEDLINE-93321614; PubMed-8330535;
                                            SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=10090
                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                  inhibin beta A chain precursor (Activin beta-A chain)
                                                                                                                                                                                                                                                                                                        425 CS 426
                                                                                                                                                                                                                                                                                                                                                                  365 SLSFHSTVINQYRLRGHNPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
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                                                                                                                                                                                                                                                                                                                                     351 CS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAES 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 QRPTLNRPVSRAALRTALQHLH-------GVPQGALLEDNREQECEIISFAET 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLAFLLLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLASCWIIVKSSPTPGSEGHSAAPNCPSCALATLPKDVPNAQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                AASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACG 350
                                                                                                                                                                                                                                                                                                                                                                                                                           HRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                              HQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQCHETGASLVLLGKKKKKEEEGEGKKKDGGEAGAGVDEEKEQSHRPFLMLQARQSEDHP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GOVAQSSVILG------GA-------AHRPF--VAARVRVGGK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSDTREEAEEADLMEERSEQLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDIRIAC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHNTNLTLATQYLLE-----VDA--SGWHQLPLGPEAQAACSQGHLTLELVLE- 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTA----RKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRSKVTIRLLQQQKHPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLSTINQTRLDFHESSDRTAGDRE-VQQASLMFFVQLPSNTTWTLKVRVLVL------G 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00250; TGF_BETA_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.3%; Score 560; DB 1; 32.5%; Pred. No. 1.7e-43;
 Smith J.C.; in preimpla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
   preimplantation mouse embryos and
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BY SIMILARITY.
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E481060B8368A77D CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                 424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 426;
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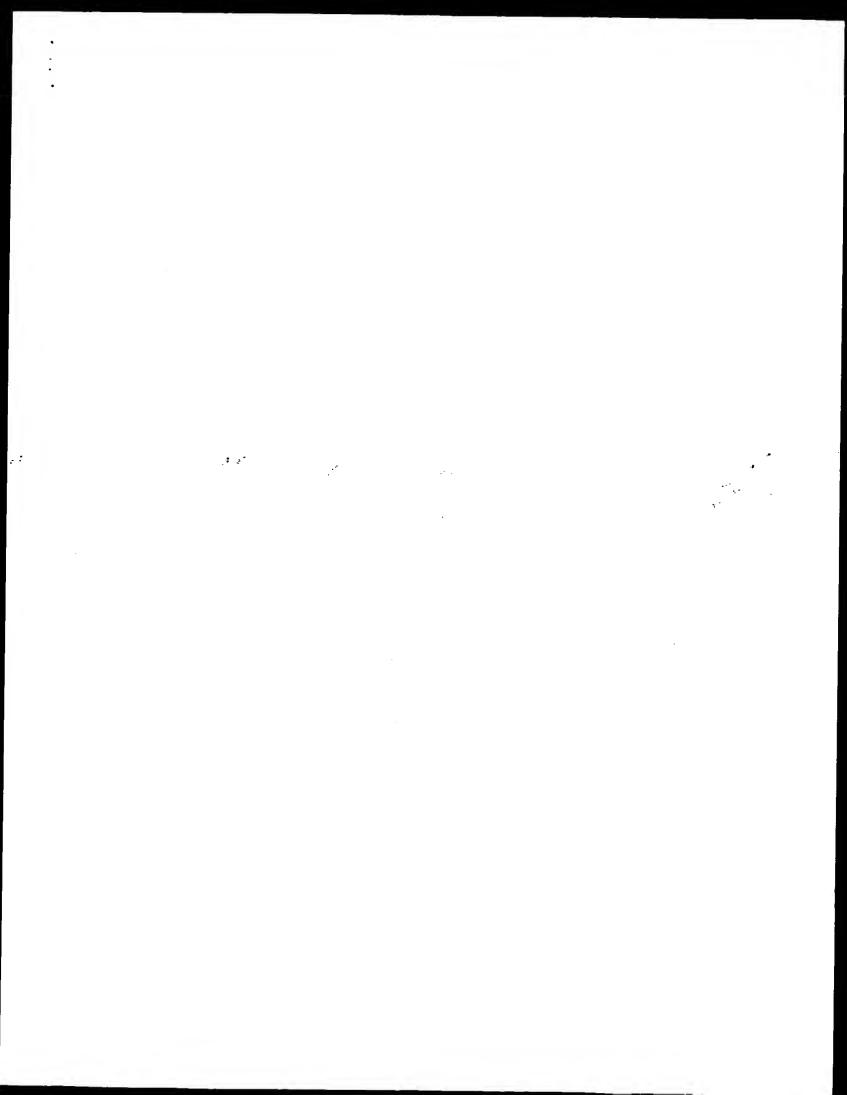
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                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GECYSKNOT.
PRINTS; PR00670; INHIBLNBA.
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P18075; 1E MGD; MGI:96570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X69619; CAA49325.1; -. PIR; S31440; S31440.
                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002400; GF_cysknot.
InterPro; IPR000491; Inhibin_betaA.
InterPro; IPR001839; TGF-beta.
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                                                                                                                                                                                                                                                                                                                                                                                       Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00204;
             159
                                        129
                                                               104 TGLSTINQTRLDFHFSSDRTAGDRE~VQQASLMFFVQLP-SNTTWT-LKVRVLVLGPH--
                                                                                        69 KKRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAE
                                                                                                                   83
                                                                                                                                              10 LLASCWIIVRSSPTPGSEGHGSAPDCPSCALATLPKDGPNSQPE-MVEAVKKHILNMLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A HOMODIMER OF BETA-B.
TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVE
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation . European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way.
                                                                                                                                                                     LLAFLLLAPTTVATPRAGG-----QCPACGGPTLELE----SQRELLLDLAKRSILDKLHL
                                                                                                                  TQRPTLNRPVSRAALRTALQHLH-------GVPQGALLEDNREQECEIISFAE 103
                                       SGTA----RKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQ
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      PS00250; TGF_BETA_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPRO01111; TGFb_N.
                                                                                                                                                                                                                                                       424
                                                                                                                                                                                                  Conservative
-----: NTNLTLATQYLLEVDASGWHQLPLGPEAOAACSQGHLTLELVLE ; | ;; ;; | | | | ; | ; | ; ; ; ;
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424
320
389
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423
388
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X
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BY SIMILARITY.
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (GLCNAC. . . ) (POTE
                                                                                                                                                                                                 Score 559; DB 1; --
Pred. No. 2.1e-43;
Prematches 135;
                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OVARY, AND LIVER.
                                                                                                                                                                                                                                                        80C251B8754A7213 CRC64;
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                                                                                                                                                                                                                            Length 424;
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                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                       80;
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MEDLINE-87005283; PubMed-3758355;
Stewart A.G., Milborrow H.M., Ring J.M., Crowth
"Human inhibin genes. Genomic characterisation
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88190086; PubMed-3267209; Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.; *Erythroid differentiation factor is encoded by the same mRNA as that of the inhibin beta A chain."; Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
                                                                                                                                                                                                                                 Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHBA_HUMAN STANDARD; PRT; 426 AA.
P08476; Q14599;
Q1-AUG-1988 (Rel. 08, Created)
Q1-AUG-1989 (Rel. 10, Last sequence update)
Q1-MAR-1989 (Rel. 11, Last annotation update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Inhibin beta A chain precursor (Activin beta-A chain) (Erythroid
                                                                                                          TISSUE-Testis;
                                                                                                                                                                                                          SEQUENCE OF 311-426 FROM N.A
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-92135888; Pubmed-1777673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-86186863; PubMed-3754442;
Mason A.J., Niall H.D., Seeburg P.H.;
"Structure of two human ovarian inhibins.";
Biochem. Blophys. Res. Commun. 135:957-964(1986).
                                                                                                                       SEQUENCE OF 311-426 FROM N.A.
                                                                                                                                                                                                                                                                                             DNA Seq. 2:103-110(1991).
                                                                                                                                                                                                                                                                                                               "Structure and sequence analysis of the human activin beta A subunit
                                                                                                                                                                                                                                                                                                                                Tanimoto K., Handa S.I., Ueno N., Murakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation protein) (EDF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 ASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 RRRRRGLECDGKVNICCKKOFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS
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                                                                                                                                                  Lett. 206:329-334(1986).
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                                                                                                                                                                         Crowther C.E., Forage R.G.;
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EMBL; X04447; CAAA8041.1; -.
EMBL; X57578; CAA40805.1; JOINED.
EMBL; X57579; CAA40806.1; -.
EMBL; X57579; CAA40806.1; -.
EMBL; AC005027; AAD43185.1; -.
EMBL; AC005027; AAD43185.1; -.
EMBL; AC040806.1; -.
EMBL; AC040806.1; -.
EMBL; AC040806.1; -.
EMBL; AC040806.1; -.
                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00019; TGF-beta; 1.
Pfam; PF000688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
PRODOM; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                          DISULFID
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                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00204; TGFB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002400; GF_cysknot.
InterPro; IPR000491; Inhihin_betaA.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P18075
MIM; 147290;
       105 GLSTINOTRLDFHFSSDRTAGDRE-VOQASLMFFVQLP-SNTTWT-LKVRVLVLGPH---
                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B23556; B23556.
PIR; S30488; S30488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                     70 KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAES 129
                                                                           59
                                                                                                      10
                                                                                                                                                                          Local
                                                                                                                       6 LLAFLLLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                ORPTLNRPVSRAALRTALQHLH-------GVPQGALLEDNREQECEIISFAET 104
                                                                                             LLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A30884; A30884.
B24248; B24248.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P18075; 1BMP
147290; -.
                                                                                                                                                                                                                                                                                                                                                                        factor;
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                        PS00250;
                                                                                                                                                                                                                  426
                                                                                                                                                           Conservative
                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                     Hormone; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                     TGF_BETA_1; 1
                                                                                                                                                                                                                                 310
426
322
391
423
423
425
390
                                                                                                                                                                                                                  47442 MW;
                                                                                                                                                                     30.1%;
                                                                                                                                                      74; Mismatches 135; Indels
                                                                                                                                                                       Score 557;
Pred. No. 3.
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                                                                                                                                                                                                                                                                     BY SIMILARITY BY SIMILARITY
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.le-43;
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Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
 SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb):
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel!
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebri
13: sp_vertebri
14: sp_unclass:
15: sp_virus:*
16: sp_bacterii
17: sp_archeap
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1849
1 MTSSLLLAFILLAPTTVATP......DSNIVKTDIPDMVVEACGCS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562222 seqs, 172994929 residues
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                                                                                                                                                                                                                                                                sp_archea:*
sp_bacteria:*
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sp_mammal:*
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sp_bacteriap:*
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sp_virus:*
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sp_rvirus:*
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                                                                        sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

Result	Score	% Query Match Length	ength	BG	ID	Description
1	688.5	37.2	367	13	Q91696	Q91696 xenopus lae
N	649	35.1	350	11	Q91XH3	Q91xh3 mus musculu
ω	607.5	32.9	370	13	Q91350	Q91350 xenopus lae
۵	584.5	31.6	395	L U	Q9PWG6	Q9pwg6 anguilla ja
ហ	573.5	31.0	393	13	090261	Q90261 brachydanio
6	564	30.5	392	13	Q9PWR8	Q9pwr8 carassius a
7	554	30.0	426	Δ.	09HBP0	Q9hbp0 homo sapien
œ	547	29.6	413	L.	098860	Q98860 cynops pyrr
φ	533	28.8	424	13	Q98SP9	Q98sp9 meleagris g
10	518	28.0	404	13	Q9PW65	
11	354	19.1	115	13	Q9DGE9	Q9dge9 cyprinus ca
12	354	19.1	119	0	Q95KP1	Q95kpl ailurus ful
13	353.5		119	13	042125	042125 pagrus majo
14	353		115	L.	Q9DGF1	Q9dgf1 cyprinus ca
15	353		115	ü	Q9DGE6	Q9dge6 oryzias lat
16	353		119	δ	Q95N79	Q95n79 ailuropoda

Query Match

37.2%; Score 688.5; DB 13; Length 367;

4 4 5 4	43	42	41	40	39	38	37	36	ა წ	ω 4	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
270 267	272	277	280	281	292.5	296.5	304.5	305	306.5	307	309.5	311	312	317	317.5	319.5	319.5	320	323	323	323.5	326	329	333	347	352	353
14.6	14.7						16.5		•			16.8	16.9	17.1	17.2	17.3	17.3	17.3		17.5	17.5	17.6	17.8		18.8	19.0	19.1
432	102	373	102	586	102	385	102	389	102	120	376	373	373	377	104	376	376	373	373	373	376	115	115	115	115	138	119
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Q95N97 Q9PTF9	Q9DET1	061643	Q90390	Q9VQG9	Q9DET3	Q90W05	Q90389	044060	Q90388	8T9M6D	Q90W06	Q98UB3	Q90ZD2	Q98TB3	198867	Q90WC8	Q90WC9	09DD18	Q90W17	Q90ZD1	Q98TB4	Q9DGE8	Q9DGF2	Q9DGE7	Q9DGF0	Q9W6T9	Q95KP2
Q95n9/ bos taurus Q9ptf9 brachydanio		O61643 drosophila		Q9vqg9 drosophila	O9det3 oncorhynchu	090w05 sparus aura	Q90389 carassius a			09w6t8 brachydanio	_	Q98ub3 salvelinus	Q90zd2 oncorhynchu	morone	cynops	morone	Q90wc9 morone saxa	Q9ddi8 salmo salar		Q90zdl oncorhynchu					09dgf0 cyprinus ca	Q9w6t9 brachydanio	Q95kp2 ursus malay

ALIGNMENTS

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SEQUENCE 367 AA; 41729 MW;	CHAIN 254 367	SIGNAL 1	W Glycoprotein; Signal.			ProDom; PD000357; TGF-	PRINTS; PRO0438; GECYSKNOT.	Pfam; PF00688;	Pfam;	InterPro; IPR00	InterPro; IPR001839;		HSSP; P12643; 3BMP.			"Molecular Cloning and functional analysis of a	Oda S., Nishimatsu S., Murakami K., Ueno N.;					Xenopodinae; Xenopus.		Eukaryota; Meta		ACTIVIN D PRECI	01-DEC-2001 (TrEMBLrel. 19,	01-NOV-1996 (TrEMBLrel. 01, Last	01-NOV-1996 (TrEMBLrel.	Q91696;	D Q91696 PRELIMINARY; PRT; 367 AA.	91696	RESULT 1

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Best Local Sim
Matches 153;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010404; AAH10404.1; -. SEQUENCE 350 AA; 39002 MW; 9B7EABAFFAC389FA CRC64;
                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91XH3
     232 QIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LIVER;
                                                                               181
                                                                                                                              123 TAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLE - VDASGWHQL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBIN BETA E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 K-HQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFGIGQCPLHIAGMP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 PRWTGWQTFSLKSMLQTFFDGGNKSLQLELNCDGCQDVPVLANPNNSHQPFLVAQAKVHE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 ITLNFQFTRDKEQ-SAHVLQAHLWLFFKANRTSQONETIRLYLVQEAYSRRILISEKLIE
                                                                                                                                                                                 66
                                                                                                                                                                                                       66 PVSRAALRTALOHLHCVPQGALLEDNREQECEIISFA---ETGLSTINOTRLDFHFSSDR 122
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 RPVSRAALRTALOHLH-GVPQGALL------EDNREQECEIISFAETGLSTINQ 111
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                                                                                                                                                                                                                                                                        6 LLAFLILLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNR 65
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                                                                                                        PLWSHHLYHARL--WLHVPPSFPGTLYLRIFRCG--TTRCRGFRTFLAEHQTTSSGWHAL 171
                                      TLPSSGLRSEDSGVVKLQLEFRPLDLNSTAAGLPRLLLDTAGQQRPFLELKIRANEPGAG
                                                                       PLGPEAQAACSOGHLTLELVLEGQVAQSS-----VILGGAA-HRPFVAARVRVG--GKH
                                                                                                                                                                          PLPQAALTRALRRLQ--PK-SMVPGNRE---KVISFATIIDKSTSTY-RSMLTFQLS--- 115
                                                                                                                                                                                                                                           GIAASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCS 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMAASFHTTVLNLIKANNI--QTAVNSCCVPTKRRPLSMLYFDRNNNVLKTDIADMIVEA
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                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                           35.1%; Score 649; DB 11; 42.4%; Pred. No. 2.7e-54; tive 58; Mismatches 118;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR002400; GF_cysknot.
InterPro: IPR001339; TGF-beta.
InterPro: IPR0011111; TGFb_N.
Pfam: PF00019; TGF-beta; 1.
Pfam: PF000688; TGFb_propeptide: 1
PFANTS; PR00438; GFCYSKNOT.
ProDom: PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
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Q91350;
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-!- SIMILARITY: BELONGS TO T
EMBL; S61773; AAB26863.1; -.
HSSP: P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
SEQUENCE 370 AA; 41679 MW; AD21502AC45F1DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dohrmann C.E., Hemmati-Brivanlou A., Thomsen G.H., Fields A., Woolf T.M., Melton D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93273083; PubMed=8500654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVIN BETA B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus
                              231 GEESHRPFLVVHARLADNKHRIRKRGLECDGHTNLCCRQQFYIDFRLIGWNDWIIAPAGY
                                                  213 GGAAHRPFVAARVRVG-GKHQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laevis."
272 AMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSCCVPTARRPLSLLY 329
                                                                                                                                                                                                  105 GLSTINQTRLDFHFSSDRTAGDRE--VQQASLMFFVQLP---SNTTWTLKVRVLVLGPHN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression of activin mRNA during early development in Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350
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                                                                                                                                                                                                                                                                  63 LNRPVSRAALRTALQHLHGVPQGALLED-------NREQECEIISFAET 104
                                                                                                                                                                                                                                                                                                        4 LLLPLLLAGLARTCAPSPTPEPGCPSC-HPPMEPE----MLEAVKRHILTLLHMQDRPN 57
                                                                                                  PDKMNMVEKKVDIRRSGWHTFPLTEAIQSLEEEGERRLNLEVQCDG-CGEYSVIPVYVDP 230
                                                                                                                                  TNLTLATQYLLEVDASGWHQLPLGPEAQAACSQG--HLTLELYLEGQVAQSSVI-----L
                                                                                                                                                                                                                                                                                                                                      LLLAFIL--LAPTTVATPRAGGOCPACGGPTLELESORELLLDLAKRSILDKLHLTORPT 62
                                                                                                                                                                    DDVTASRVRLSFTIANE----GNQNLFVFQSNLWLYLKLPEVMDKSRRKIRIKVHFQDAFN
                                                                                                                                                                                                                                      ITHMVPRAAMVSALRKLHA---GRVREDGNLEIPDLDGHSLPPPGHSTENSAEIITFAET 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RARRETPTCEPETPLCCREDHYVDFQELGWEDWILQPEGYQLNYCSGQCPPHLAGSPGIA
                                                                                                                                                                                                                                                                                                                                                                             140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASFHSAVESLLKANNP--WPAGSSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 349
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       32.9%; Score 607.5; DB 36.6%; Pred. No. 3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                          70;
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                                                                                                                                                                                                                                                                                                                                                                        Mismatches 122; Indels
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Best Local Similarity
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00671; INHIBINBC.
PRINTS; PR00672; INHIBINBC.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000381; Inhibin_betaB.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anguilla japonica (Japanese eel).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Anguillidae; Anguilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVIN B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P12643; 3BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7937
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348 FDDEYNIVKRDVPNMIVDECGCA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 LRTALQHLHGVPQGALLEDNR-------EQECEIISFAETGLSTINQTRL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 APGTETQTVSQDTCASCGLGQPEESGRMDIDFLEAVKRHILNRLQMRERPNITHPIPKAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                  NYCEGSCPAYMAGVPSSASSFHTAVVNQYRMR----GMSPGSMNSCCIPTRLSTMSMLYFD
                                                                                    NFCIGOCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSCCVPTARRPLSLLYYD 331
                                                                                                                                                                                                                                                                                 GRWGLVEKRVELKRSGWHTFPLTEPVRGVFERGDRRQDLDVRCEGCEAAAVLPVLVDPGD 257
                                                                                                                                                                                                                                                                                                                                               -----TOYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVIL------GG 214
                                                                                                                                                                                                                                                                                                                                                                                                                 SFHFLISNEGNONLYVSQASLWLYFRLLPSASEKGSRRKVTVKVYYQQTGAAAAAAAAA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFHF-SSDRTAGDREVQQASL-MFFVQLP-----SNTTWTLKVRVLVLGPHNTNLTLA- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVTALRKLHA---GKVREDGRVEIPNLDGHATYNNEVQEDTSEIISFAES--DELTSSKS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APTTVATPRAGGQCPACGGPTLELESQREL-LLDLAKRSILDKLHLTQRPTLNRPVSRAA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 AA; 43889 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.6%; Score 584.5; DB 1 35.2%; Pred. No. 5.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FA56DD62D18509A3 CRC64;
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                                                                                                                                                     317
                                374
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Q90261
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Query Match
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InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
InterPro; IPR001111; TGFb_L.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PFANTY; PR00438; GFCYSKNOT.
PRODOM; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Disruption at mesoderm and axis formation in fish by ectopic expression of activin variants: the role of maternal activin. Genes Dev. 8:1448-1462(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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363 LSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 393
                                                                                                                                                                 264 WIIQPEGYAMNECIGQCPLHIAGMPGIAASEHTAVLNLLKANTAAGTTGG--GSCCVPTA 321
                                                                                                                                                                                                                                                                                                                                           187 SYEPGGONVHWPM-MEKRVELKRSGWHTFPVSEAIREMLAKGGRRODLDIHCEGCEAANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 MRERPNITHPIPKAAMVTALRKLHA---GKVREDGRVEIPNLDGHAAHNEVQEETSEIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTSSLLLAFLLLAPTTVATPRAG···GQCPACGGPTLELESQREL-LLDLAKRSILDKLH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSVTCLMACLLSVQCSSLGAETGSQESQCVSCGLGHQEDSGRMDTDFLEAVKRHILNRLQ
                                                      RRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                             WITAPAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQYRMR----GMSPGSVNSCCIPTK
                                                                                                                                                                                                                             LPILVDPSDPSHRPFLVVRAQQADGKHRIRKRGLECDGNNGGLCCRQQFYIDFRLIGWND
                                                                                                                                                                                                                                                                              L-----GGAAHRPFVAARV-RVGGKHQIHRRGIDCQGGS-RMCCRQEFFVDFREIGWHD
                                                                                                                                                                                                                                                                                                                                                                                                  ----GPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAESDDVTPSKSSLYFLISNE---GNQNLYVLQANLWLYFKLMPGTLEKGLRAKVTVRVH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAETGLSTINQTRLDFHFSSDRTAGDRE--VQQASL-MFFVQLPSNTTWTLKVRVLVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZDB-GENE-990415-2; inhbb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.0%; Score 573.5; DB 13; Length 393; 34.3%; Pred. No. 6.2e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
Pfam; PF00671; INTIBINBB.
PRINTS; PR00672; INTIBINBC.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ge W., Miura T., Kobayashi H., Peter R.E., Nagahama Y.;

"Cloning of cDNA for goldfish activin beta B subunit, and the
expression of its mRNA in gonadal and non-gonadal tissues.";

J. Mol. Endocrinol. 19:37-45(1997).

1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL; AF004669; AAB61468.1;

HSSP; P12643; 3BMP.

InterPro; IPR000381; Inhibin_betaB.

InterPro; IPR001318; Inhibin_betaC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9PWR8;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACTIVIN BETA B SUBUNIT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Meopterygli; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID-7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97424746; PubMed=9278859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001839; TGF-beta.
                                                                                                                                                                                                                                                    246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 RERPNITHPIPKAAMVTALRKLHA---GKVREDGRVEIPNFDGHAAHNEVQEETSEIISF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTSSLLLAFILLAPTTVA--TPRAGGQCPACG-GPTLELESQRELLLDLAKRSILDKLHL
                                 RPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
STMSMLYFDDEYNIVKRDVPNMIVEECGCA 392
                                                                                                                                                                     IIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGG--GSCCVPTAR
                                                                                                                                                                                                                                  PILVDPSDPSHRPFLVVRAQQADSKHRIRKRGLECDGTNGGLCCRQQFYIDFRLIGWNDW
                                                                                                                                                                                                                                                                                         -----GGAAHRPEVAARV-RVGGKHQIHRRGIDCQG-GSRMCCRQEFFVDFREIGWHDW
                                                                                                                                                                                                                                                                                                                                                         YEPGGQNVHWPM-MEKRVELKRSGWHTFPVSEAVREMLAKGGRRQDLDIHCEGCEAANVL
                                                                                                                                                                                                                                                                                                                                                                                                                LVLGPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVIL 212
                                                                                                                    IIAPAGYYGNYCEGSCPAYMAGYPGSASSFHTAVVNQYRMR---GISPGSVNSCCIPTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AESDDVTPSKSSLYFLISNE·--GNQNLYVLQANLWLYFKLLPGTQEKGLRRKVTVRVRS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AETGLSTINOTRLDFHFSSDRTAGDRE--VQQASL-MFFVQLPS-----NTTWTLKVRV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSVTCLMACILSVQCSLGAETVSQESQCASCGLGHPDDSGRMDTDFLEAVKRHILNRLQM 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
392 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.5%; Score 564; 34.1%; Pred. No. 5.
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; 73AAA7E1C0B2450B CRC64;
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.1e-46;
es 130; Indels 4
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Best Local
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PRINTS; PR00670; INHIBINBA.
PRINTS; PR00672; INHIBINBA.
PRINTS; PR00672; INHIBINBC.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9HBPO;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 47.5 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel Human cDNA clones with function
growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Hypothetical protein.
SEQUENCE 426 AA; 47454 MW; 339276317BD5B408 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases -- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gu J.R., Wan D.F., Zhao X.T.,
Qin W.X., Huang Y., Qiu X.K.,
                                                                                                                                                                        204
                                                                                                                                                                                                          185
                                                                                                                                                                                                                                                                         130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: AF218018; AAG17260.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; vertebrata; висете
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09нвр0
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                               291 AASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACG
                                                                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LLAFLLLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
SLSTHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG
                                                                                   HQIHRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGI
                                                                                                                                                                                                                                                                 GTA----RKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQG
                                                                                                                                   EQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHP
                                                                                                                                                                   QVAQSS----VILG------GA-----AHRPF--VAARVRVGGK 230
                                                                                                                                                                                                   SLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDVRIAC
                                                                                                                                                                                                                                                                                                  GLSTINQTRLDFHFSSDRTAGDRE-VQQASLMFFVQLP-SNTTWT-LKVRVLVLGPH---
                                                                                                                                                                                                                                                                                                                                                                   QRPTLNRPVSRAALRTALQHLH-------GVPQGALLEDNREQECEIISFAET 104
                                                                                                                                                                                                                                                                                                                                                                                                   LLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                  HRRRRGLECDGKVNICCKKOFFYSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGS
                                                                                                                                                                                                                                 --------NTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEG
                                                                                                                                                                                                                                                                                                                                    KRPDVIQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAES 129
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IPR000491; Inhibin_betaA.
IPR001318; Inhibin_betaC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 554; 31.5%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
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Qian L.F., He L.P., Li H.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 135;
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                                                                                                                                                                                                                                                                                                                                                      ENTRY
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                                                                                                                                                                                                                    ACCESSIONS
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                                                                                                                               #journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 qniikkdiqnmiveecgcs 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 NFCIGQCFLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **molecule_type protein

**residues 309-311,'x',313-318,'xx',321-325 **label AL2

FICATION *superfamily inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:X69619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 shrpflmlgarqsedhphrrrrrglecdgkvnicckkqffvsfkdigvndwiiapsgyha 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 nycegecpshiagtsgsslsfhstvinhyrmrghspfanlksccvptklrpmsmlyyddg 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 AHRPEVAARVRVGGKH-QIHRR-GIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAM 273
                                                                                                                                                                                                                                                                                                                                                                                                                                             334 SNIVKTDIPDMVVEACGCS 352
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Local Similarity 47.5%;
**molecule_type DNA
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Inhibin beta-A chain - mouse
activin A; mesoderm-inducing factor WEHI-MIF
activin A; mesoderm-inducing factor WEHI-MIF
#formal_name Mus musculus #common_name house mouse
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack, J.M.W.; Smith, J.C. Development (1990) 110:435-443
A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia cells is activin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S31440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *length 424 *molecular-weight 47392 *checksum 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1992
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                                                                                                                                                                                                                                                       inhibin beta-A chain precursor - bovine activin; mesoderm inducing factor *formal_name Bos primigenius taurus *common_name cattle 01-Aug-1995 *sequence_revision 01-Sep-1995 *text_change
                                                           Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. (1994) 256:751-764
Genomic cloning and sequence analyses of the bovine alpha-,
beta(A)- and beta(B)-inhibin/activin genes. Identificatio
of transcription factor AP-2-binding sites in the
5'-flanking regions by DNase I footprinting.
                                              850898
                                                                                                                                                                                                                    S50898; B25732; A60960; B61548
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                                                                                                                                                                                                                                                                                                                                                                                         SERVIENCE COMPANYSON A
                     preliminary
                                                                                                                                                                                                                                                                                                                                                      *type complete
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                                                                                                             Identification
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                                                               ALTERNATE_NAMES
                                                                                                                                 RESULT
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310-425
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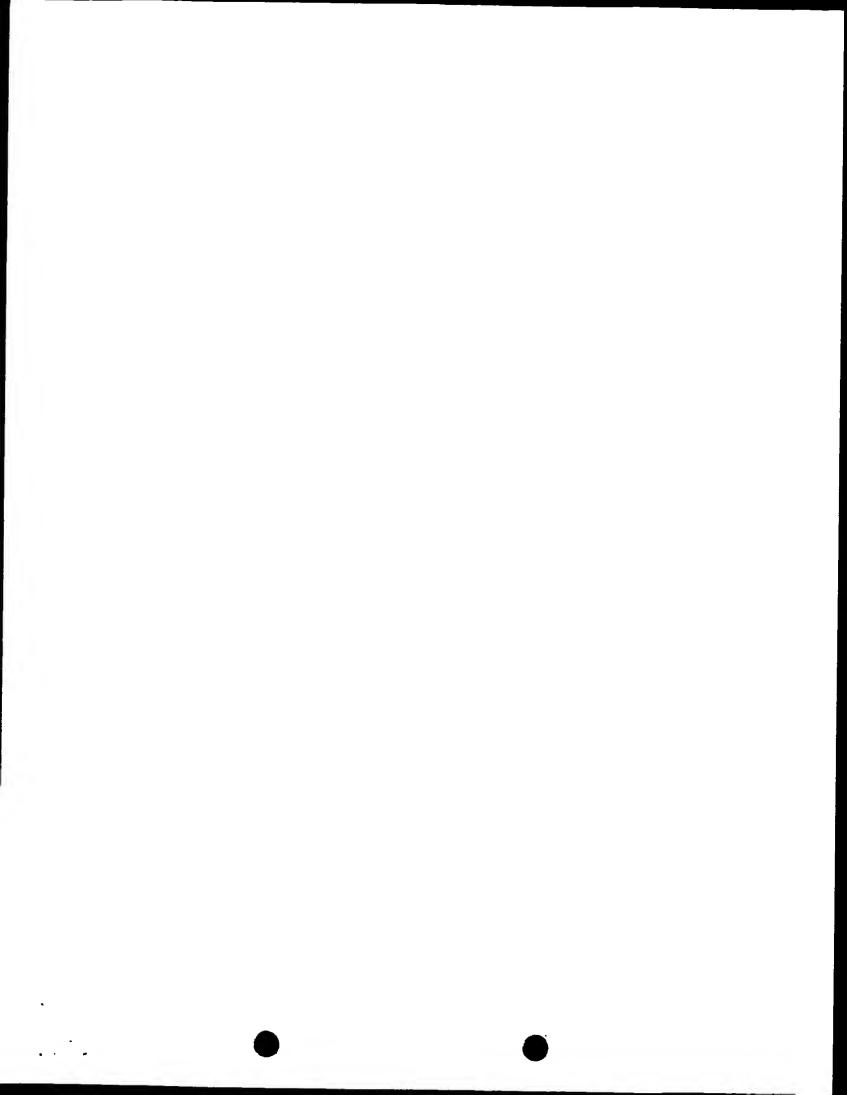
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B24248 *type complete
Inhibin beta-A chain precursor - human
activin A; activin AB chain A; erythroid differentiation
factor; megakaryocyte differentiation active protein
*formal_name Homo sapiens *common_name man
21-May-1988 *sequence_revision 21-May-1988 *text_change

06-Sep-1996

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*introns
CLASSIFICATION
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#title Cloning and sequence analysis of cDNA species coding for the
two subunits of inhibin from bovine follicular fluid.
#cross-references_MUID:86205842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type protein
##residues 310-312, 'X', 314-319, 'XX', 322-328, 'P' ##label CHE
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##residues 310-313 ##label FUK
                                                                                                                                                                                                                                         **residues
                                                                                                     274 NFCIGOCFLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLXXDRD 333
334 SNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                     Match 21.3%;
Local Similarity 47.5%;
                             qniikkdiqnmiveecgcs 425
                                                                                                                                                     nycegecpshiagtsgsslsfhstvinhyrmrghapfanlksccvptklrpmsmlyyddg 406
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Biomed. Sci. (1990) 1:499-506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A61548 Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesoderm-inducing factor from bovine amniotic fluid: purification and N-terminal amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily inhibin
disulfide bond; glycoprotein; gonad; heterodimer; homodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #length 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation of bovine follicular fluid inhibin of about 32 kDa
                                                                                                                                                                                                                                                                                                                                                                Conservative
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part of this sequence, including the amino end of the
mature protein, was confirmed by protein sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product beta-A inhibin/activin #status experimental
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *molecular-weight 47521 *checksum 898
                                                                                                                                                                                                                                                                                                                                                             Score 543; DB 6; Length 425; pred. No. 1.13e-76; 30; Mismatches 41; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID-8330;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFC_SKNOT.
PRINTS; PR00670; INHIBINBA.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
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InterPro: IPR001839; TGF-beta.
InterPro: IPR001111; TGFb_N.
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SEQUENCE 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 AG-----OSKKYLHFEISKEGSDLSLYEQAEFWLFYKLNKSNRSRTKLTIRLYQQQQRGQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 TGLSTINQTRLDFHFSSDRTAGDRE-VQQASLMFFVQLPSNTTWTLKVRVLVL----- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 ----GPHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSS- 209
                                                                                                                                                                                                                                                       245 ATPTLLCKKKKKEEEVKAANGSAGDEEREQSHRPFLMIMARQSEEHPHRRRKRGLECDGK 304
                                                                                                                                                                                                                                                                                                                         210 ---VILG------GAA------HRPF--VAARVRVGGKHQIHRRGIDCQGG 243
                                                                                                                                                                                                                                                                                                                                                                                     185 DEERGQERDKKEVLIAEKTLDTKRSGWHTFNIAKSIQHLLDQGKTSLDIRIACDQCQETG 244
                                                              304 ANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGGS 352
                                                                                                                             305 VSICCKKQFYVSFKDIGWSDWVIAPPGYTANYCEGDCPMYITGTSGSGPSFHAAVINQYR 364
                                                                                                                                                                                     244 SRMCCROEFFVDFREIGWHDWIIOPEGYAMNFCIGOCPLHIAGMPGIAASFHTAVLNLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLLGLCWIATRASPTPGTEGQGSVTDCPSCALGRLEKAAPSSQADMVEAVKKHILSMLHM 69
365 MRGYSPFTSVKSCCVPTKLRAMSMLYYDDGQNIIKKDIONMVVEECGCS 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TORPTLNRPVSRAALRTALOHLH----GVPQGALLEDN------REQECEIISFAE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LLLAFLLLAPTTVATPRAGGO-----CPACGGPTLE--LESQRELLLDLAKRSILDKLHL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSRPNITQPVPKAALLNAIKKLHVGKVGQDGYVEIEDDVGRRAERSELLEQTSEIITFAE 129
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of turkey inhibin-alpha and betaA subunits.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL, AF336338; AAK21265.1; -.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Cranie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q98SP9
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Prodom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00669; INHIBINA.
PRINTS; PR00670; INHIBINBA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001839; TGF-beti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002405; Inhibin_alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                              130 G--TPKKT---LHFEISKEGSELSVVEHAEVWLELKVSKANRSRTKVTIRLFOQQRQPKG 184
                                                                                                                                                                                              185 NSEGSEDMEDGGLKGERSETLISEKAVDTRKSTWHIFPVSSSVQRLLDQGKSSLDVRIAC 244
                                                                                                                                                                                                                            159 ------NTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEG 203
                                                                                                                                                                                                                                                                                            105 GLSTINOTRLDEHFSSDRTAGDRE-VQQASLMFFVQLPSNTTWTLKVRVLVLGPH---- 158
                              293 SFHTAVLNLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                 305 RRKRGLECDGKVNICCKKOFFVSFKDIGWSDWIIAPTGYHANYCEGECPSHIAGTSGSSL 364
                                                                                              233 IHRRGIDCOGGSRMCCRQEFFVDFREIGWHDWIIOPEGYAMNFCIGOCPLHIAGMPGIAA 292
                                                                                                                                245 DLÇQETGASLVLLGKKKKKEDDGEGKEKDAGELTGEEEKEQSHRPFLMMLARHSEDROHR 304
                                                                                                                                                              204 QVAQ----SSVILG-------GAAHRPF--VAARVRVGGKHQ
365 STHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS 424
                                                                                                                                                                                                                                                                                                                                                                                              10 LLVICWIIVRSSPTPGSEGHSSVTDCPSCALTTLSKDVPSSQPEMVEAVKKHILNMLHLR 69
                                                                                                                                                                                                                                                                                                                              70 DRPNITQPVPKAALLNAINKLHVGKVGDDGYVEIEDDVGRIAQMNEVVEQTSEIITFAQS 129
                                                                                                                                                                                                                                                                                                                                                          59 QRPTLNRPVSRAALRTALQHLH-------GVPQGALLEDNREQECEIISFAET 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            6 LLAFLLLAPTTVATPRAGG-----QCPACGGPTL--ELESQRELLLDLAKRSILDKLHLT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 AA; 47442 MW; B3E7CF3B9FDF0C59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.8%; Score 533; DB 13; Length 424;
30.5%; Pred. No. 5.6e-43;
tive 69; Mismatches 145; Indels 78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibin_betaC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibin_betaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 AA
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                      Q9DGE9
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Best Local
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InterPro; IPRO00491; Inhibin_betaA.
InterPro; IPRO01839; TGF-beta.
InterPro; IPRO01111; TGFb_N.
Pfam; PF00619; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
Pfam; PF00689; INHIBINA.
PRINTS; PR00659; INHIBINA.
PRINTS; PR00670; INHIBINA.
PRINTS; PR00670; INHIBINA.
PRINTS; SM00204; TGFb; 1.
SMART; SM00204; TGFB; 1.
        Q9DGE9
                                                                        373 RLRAMSMLYYNEEQKIIKKDIQNMIVEECGCS 404
                                                                                                     321 ARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                            261 WHDWIIOPEGYAMNFCIGOCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSCCVPT 320
                                                                                                                                                                                            253 VPTESNKGKEREQSHRPFLMVVLKPAEEHPHRRSKRGLECDGKIRVCCKRQFYVNFKDIG
                                                                                                                                                                                                                        216 -----AHRPEVAARVRVGGKHQIHR--RGIDCQGGSRMCCRQEFFVDFREIG 260
                                                                                                                                                                                                                                                      204 EKTVDTRRSGWHTLPVS------RTVQTLLDGDSSMLSLRVSCPMCAEAGAVPIL 252
                                                                                                                                                                                                                                                                                       167 QYLLEVDASGWHOLPLGPEAQAACSQGHLTLELVLEGQVAQSSVIL-----GGA---- 215
                                                                                                                                                                                                                                                                                                                    150 MEGNTLS---VVEQANVMLLLKVAKGSRGKGKVSVQLLQHGKADPGSADGPQE---AVVS 203
                                                                                                                                                                                                                                                                                                                                                    118 FSSDRTAGDREVQQASIMFFVQLPSNTTWTLKVRVLVL-------GPHNTNLTLAT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN, PITUITARY;

Yam K.M., Yu K.L., Ge W.;

"Cloning and characterization of activin beta A subunit.";

MO1. Cell. Endocrinol. 0:0-0(1999).

-I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL; AF169032; AAD50448.1;

-HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PW65;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACTIVIN BETA A PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Ncopterygii; Teleostei; Euteleostei; Ostariophysi Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                 73 RTALQHLH------GVPQGALLEDNREQECEIISFAETGLSTINOTRLDFH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                 91 LNAIRRLHVGRVGEDGTVEMEEDGGGLGEHREQSEEOPFEIITFAEPG-DAPDIMKFDIS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                              36 PDDPVTP----CPSCALAQRQKDSEEQTDMVEAVKRHILNMLHLNTRPNVTHPVPRAAL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 PTTVATPRAGGOCPACGGPTLELESQREL-LLDLAKRSILDKLHLTQRPTLNRPVSRAAL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PW65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                             WSDWIIAPSGYHANYCEGDCPSHVASITGSALSFHSTVINHYRMRGYSPENNIKSCCVPT 372
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 AA; 44799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%; Score 518; DB 13; 30.9%; Pred. No. 1.5e-41; tive 68; Mismatches 127;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVIN BETA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3AFB41BE62A8CODC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ostariophysi;
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                                                                                                                                          Matches
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                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095KP1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                237 GIDCOGGSRMCCROEFFVDFREIGWHDWIIQPEGVAMNFCIGQCPLHIAGMPGIAASFHT 296
                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                EMBL; AY029555; AAK40342.1; -.
                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of the activin gene A subunit mature peptide from panda related animals.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ailurus fulgens (Lesser panda).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVIN SUBUNIT A (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang X., Wang Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Ailurus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q95KP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Tada T., Hirono I., Aoki T., Takashima F.;

Toloning and sequencing of carp and medaka activin subunit genes.";

Pisheries Sci. 64:680:685(2000).

-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

BMBL: AB009406; BAB17599.1;

HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9DGE9; O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INHIBIN/ACTIVIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00669; INHIBINA. ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002405; Inhibin_alpha
InterPro; IPR001839; TGF-beta.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 TAVLNILKANTAAGTTGG--GSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein.
3 GLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHS 62
                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 GIDCOG-GSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TAVVNQYRMR---GMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLECDGTNGGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCPAYLAGVPGSASSFH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 AA;
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                  119; 13328 MW; 0A319B2F25D83CB6 CRC64;
                                                                                                                                                19.1%; Score 354; DB 6 50.4%; Pred. No. 2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12666 MW; CD38FA0DD7BD52A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.1%; Score 354; DB 13; 51.7%; Pred. No. 1.9e-26;
                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AA.
                                                                                                                                                                       DB 6; Length 119;
                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                  0;
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                                                                                                         Gaps
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09DGF1
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Best Local
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042125;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACTIVIN BETA B (FRAGMENT).
Pagrus major (Red sea bream) (Chrysophrys major).
Eukaryota; Metezoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidel; Sparidae; Pagrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta; 1.
probom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGE_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-OVERY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-143350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygil; Neopterygil; Teleostel;
Cypriniformes; Cyprinidae; Cyprinus.
NCBL_TaxID-7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001839; TGF-beta.
SEQUENCE FROM N.A.

Tada T., Hirono I., Aoki T., Takashima F.;

"Cloning and sequencing of carp and medaka activin subunit genes.";

Fisherics Sci. 64:680-685(2000).

-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL. AB009404: BAB17597.1;

HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INHIBIN/ACTIVIN (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DGF1;
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InterPro; IPR001839; TGF-beta.
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OSDGE6:
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INHIBIN/ACTIVIN (FRAGMENT).
Oryzias latipes (Medaka fish).
Oryzias latipes (Medaka fish).
Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostomi;
Acanthomorpha; Acanthopterygii; Peleostel; Euteleostel; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzilnae; Oryzlas.
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ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mosses 1 to 1558)

1 (bases 1 to 1558)
Hoetten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
HOVEL GROWTH OR DIFFERENTIATION FACTOR OF THE TGF- beta FAMILY
Patent: WO 9601316-A 3 18-JAN-1996;
Patent: WO 9601316-A 3 18-JAN-1996;
                                                                                                    BIOPHARM GES ZUR BIOTECHNOLOGI (DE)
Other publication AU 2979895 960125
Other publication DE 19511243 960104
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1 (bases 1 to 1558)
Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
DNA encoding growth/differentiation factor
Patent: US 5807713-A 3 15-SEP-1998;
Location/Qualifiers
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                    GCGCCTCCGCGGGCCTCGACGGGAAACCCCTGTTGGAGCATGACCAGAGACAAGAAGAATA 420
                                             CAGCCAGCGCCCATACTCAGTCGGCCAGTGTCCAGAGGGGCTCTCAAGACCGCGCTGCA
AR123395
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Hotten,G., Neidhardt,H., Bechtold,R., Pohl,J. an Method of treatment with growth/differentiation TGF-.beta. family
                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-.beta. family Patent: US 6171584-A 3 09-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structure, chromosomal localization, and expression analysis of the mouse inhibin/activin beta C (Inhbc) gene Genomics 32 (3), 358-366 (1996)
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/db_xref="MGD:MOI:105932"
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/translation="MASSLILALIFITTVVNPKTEGPCPACWGAIFDLESORELLL
DLAKKSILDKLHLSGRPILSRPVSRGALKTALQRLRGPRRETLLEHDORQESYEIISF
ADTDLSSINGTRLEFHFSGRMASGMEVROTRPWFFVQFPHNATOTMIRVLVLRPYDT
MLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHR
PFVAAQVKVEGKHRVRRRGIDCQGGSEMCCRQEFFVDFREIGWNDWIIQPEGYAMNFC
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/protein_id="CAA62333.1"
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/tissue_type="liver"
/dev_stage="adult"
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/db_xref="taxon:10090"
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Direct Submission
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Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                      Submitted (16-AUG-1995) H. Schrewe, Max-Planck-Institut fuer Immunibiologie, Postfach 1169, D-79011 Freiburg, FRG 2 (bases 1 to 2049) Schmitt, J., Hotten, G., Jenkins, N.A., Gilbert, D.J., Copeland, Pohl, J. and Schrewe, H.
                                                                                                                                                                                                                                             Genomics 32 (3), 358-366 (1996)
                                                                                                                                                                                                                                                           Structure, chromosomal localization, mouse inhibin/activin beta C (Inhbc)
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Submitted (16-NOV-1995) Anthony L. Lau,
of Medicine, One Baylor Plaza, Houston,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Lau,A.L., Nishimori,K. and Matzuk,M.M.
Structural analysis of the mouse activin beta C
Biochim. Biophys. Acta 1307 (2), 145-148 (1996)
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/product="activin beta-C precursor"
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/db_rtein_id="acc52723.1"
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488. .838
/product="activin beta-C"
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/db_xref="taxon:10090"
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97.1%;
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                                                                                                                                                               TAAGCTAGAGGCTAATCGACTGCCTACCACAAGCAATGTCATTTTGTTCCTGGCAAACAC 1114
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                                                                                                                                                                                                             TGACCAACAGCCTTTCTCTCTCCTGGGACATGGTTGACCCCAGTACACCCATCCTCAGCCT 1054
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551 CCCCACAATGCCACCCAGACCATGAATATAAGAGTTCTTGTGCTAAGACCATATGACACC
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Submitted (01-APR-1999) Institute of Cancer Research,
Vienna, Borschkegasse Ba, Vienna A-1090, Austria
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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/product="activin beta C"
/protein_id="AAD30132.1"
/db_xref="GI:4809187"
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Other publication AU 2979895 960125
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               GTGGCATGGAGGTCCGGCAGACCCGCTTCATGTTCTTCGTGCAGTTCCCCCACAATGCCA 563
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Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
DNA encoding growth/differentiation factor
Patent: US 5807713-A 1 15-SEP-1998;
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Patent: US 6171584-A 1 09-JAN-2001;
Location/Qualifiers
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Hotten,G., Neidhardt,H., Bechtold,R., Pohl,J. and Paulista,M. Method of treatment with growth/differentiation factors of the
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 CTTGGACCTTGAAAGTGAGAGTCCTTGTGCTGGGTCCACATAATACCAACCTCACCTTGG
           CCCAGACCATGAATATAAGAGTTCTTGTGCTAAGACCATATGACACCAACCTCACCTTGA 623
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2272)

H tten,G., Neidhardt,H., Schneider,C. and Pohl,J.

Cloning of a new member of the TGF-beta family: a putative new activin beta C chain
                                                                                      Submitted (07-NOV-1994) G. Hoetten,
                                                                                                                                                Biochem. Biophys. Res. Commun. 206 (2), 608-613 (1995)
                                                                                                                                                                                                                                                            x82540.1 GI:669154
activin beta-C chain; activin beta-C gene
                                                                                                     Direct Submission
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                                                                                                                                                                                                                                          Homo sapiens
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/organism="Homo sapiens"
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/tlssue_type="liver"
/clone_lib="liver cDNA (Clontech)"
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/translation="MTSSLLAFTLLAFTLVATPRAGGOCPACGGPTLELESORELLL
/translation="MTSSLLAFTLLAFTLVATPRAGGOCPACGGPTLELESORELLL
DLAKRSILDKLHLTORFTLNRPVSRAALTRACHHHGVPORALLEDNREOGECELISFA
ETGLSTINOTRLDEHFSSDRTAGDREVQQASLMFFVQLPSNTTWTLKYRVLVLGPHNT
NLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELYLEGQVAQSSVILGGAAHR
PFVAARVIVGGKHQLHRRGIDCOGGSBMCCROEFFVDFREIGWHDNIIQPEGYAMNFC
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/protein_id+"CAA57890.1"
/db_xref="GI:669155"
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                                                                                                                   /protein_id="CAC33330.1"
/protein_id="CAC33330.1"
/db_xref="GI:13185365"
/translation="MTSSLLLAFTLLLAPTYVATPRAGGOCPACGGPTLELESORELLL
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NLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGOVAQSSVILGGAAHR
PFVAARVHVGGKHQIHRRGIDCQGGSRNCCROEFFVDFREJWHDWIIGTIATVANDROC
                                                                         IGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSXCVPTARRPLSLLYYDRDS
NIVKTDIPDMVVEACGCS"
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0; Mismatches 238;
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                                                                              TAAGGGTTGAGGGCAAGCATCGGGTTCGCCGGCGAGGTATCGATTGCCAGGGGGGGTCCA
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                                                        GCCCAGCATGTTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGAGCTGCTTCTCGATT 266
                                                                                                                                                   TGGCCAAGAGAAGCATCTTGGACAAGCTGCACCTCACCCAGCGCCCAACACTGAACCGCC •323
                                                                                          GTCCAGCATGTGGGGGGGCCCACCTTGGAACTGGAGAGCCAGCGGGAGCTGCTTCTTGATC
                                                                                                                                                                                  TCCTGGCTCTTCTGTTCCTGACTCCAACCACCACTAGTGAACCCCAAAACTGAGGGTCCAT
                                                                                                                                                                                                              CTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC 143
                                                                                                                                                                                                                                             CTGAATATAGGCTTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTCCTTGC 146
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/db_xref="taxon:9606"
128. .1186
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/db_xref="GI:14273977"
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Search completed: October 11, 2002, 23:57:40 Job time: 1946.25 secs

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1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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6: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA198.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA198.DAT:*
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27: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match Length DB ID Match Length DB ID 94.3 1837 19 AAV38237 65.8 10708 19 AAV69286 50.0 2272 17 AAF11104 49.9 2272 22 AAF74421 13.6 265 14 AAQ47710 10.9 5099 19 AAV38239 9.3 2125 19 AAV38239 9.3 2125 19 AAV38239 9.3 2125 19 AAV38239 9.3 2125 19 AAV38239
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ALIGNMENTS

RESULT 1 AAV38237 Murine liver activin beta c polypeptide encoding cDNA. AAV38237; AAV38237 standard; cDNA; 1837 BP 01-FEB-1999 (first entry)

Liver activin; beta c; beta e; cell differentiation; haematopolesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropolesis; haemophilia; cystic fibrosis; immunoasse menstrual disorder; transgenic; modulator; ss. immunoassay;

Mus sp.

FTT FTH XXX CDS sig_peptide mat_peptide 20-NOV-1997; 28-MAY-1998. WO9822492-A1. 97WO-US20882. /*tag= b 209..1204 /product- "activin beta c polypeptide" 149..208 Location/Qualifiers 149..1207 /*tag= a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC derived from beta c cDNA clone is used for screening and cloning a liver activin beta e gene. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene conditions and cloning a liver activin beta e gene. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene conditions of haematopolesis, erythroid differentiation, ovarian follicular conformation, insulin secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions can be diagnosed using the liver activin. Cell growth and compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to compound may also induce bone growth (e.g. for treating osteoporosis or treating haematopolesis, particularly erythropolesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce or the transgenic animals, are useful for screening for liver activin. Also, the transgenic animals, are useful for screening for liver activin.
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Best Local Similarity
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Sequence 1837 BP; 418 A; 531 C; 455 G; 433 T; 0 other;
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                                                                                                          "CAGCCAGCGCCCCATACTCAGTCGGCCAGTGTCCAGGGGGCTCTCAAGACCGCGCTGC 359
                                                                       AGAGCCAGCGGGAGCTGCTTCTCGATTTGGCCAAGAAAGTATCCTGGACAAGCTGCACC
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                                   1458 GTCATTTTGTTCCTAGCAAACACACCCTTAGCTCTCCCTTAGTCAACTATGTAATCTACT
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                                                  TGTCATTTTGTCCTAGCAAACAC-CCCTTAGCTC-CCCTTAGTCAACTATGTAATCTACT 1492
                                                                                                     CCCAGTACACCCATCCTCAGCCTTAAGTTAGAGGCTAATCGACTGCCTACCACAAGCAAT
                                                                                                                                     CCCAGTACACCCATCCTCAGCCTTAAGTTAGAGGCTAATCGA----CTCCTACATATATA 1434
                                                                                                                                                                      TGTCCAGAATGGAAACACCTTTCTAAGCATGCAGACATCCCCTCTGTGGACTTCAGGGGAT 1337
                                                                                                                                                                                                                                                              TGTCCAGAATGGAAACACCTTTCTAAGCATGCAGACATCCCTCTGTGGACTTCAGGGGAT 1318
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Liver activin; beta c; beta e; cell differentiation; haematopolesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropolesis; haemophilia; cystic fibrosis; immunoassay; menstrual disorder; transgenic; modulator; ss.
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WPI; 1998-312408/27. P-PSDB; AAW60617, AAW60618.

New isolated nucleic acid encoding sub-units of liver activin useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoletic disorders

Disclosure; Fig 4D-G; 141pp; English.

CC insulin secretion, neuronal survival, spermatugenesis, bone formation, cainsulin secretion, neuronal survival, spermatugenesis, bone formation, coinsulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can compound the sexpression. Antagonists can be used to treat cupregulates the compound's expression. Antagonists can be used to treat colliver diseases while agonists can be used to increase growth and correspond to the second of the liver tissue. The liver activin compound may also induce compound to the second of compound to the second of consequences of the second of the seco This cDNA encodes a murine liver activin beta c polypeptide. Sequences CC derived from beta c cDNA clone is used for screening and cloning a liver activin beta e gene. Disorders of cell growth or differentiation (or CC susceptibility to them) are diagnosed by measuring liver activin gene cactivity or by detecting a mutation in the liver activin gene. Disorders CC activity or by detecting a mutation in the liver activin gene. Disorders CC increase in the liver activin gene conditions can be diagnosed using the liver activin. Overlan follicular CC compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to compound may also induce bone growth (e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies care useful in immunoassays, to generate anti-idiotypic antibodies'(which liver activin receptors) and to inhibit liver activin. Also, the liver activin containing liver activin gene can be used to produce transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, containing liver activin gene activin. them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopoiesis, erythroid differentiation, ovarian follicular maturation, This represents the sequence of mouse activin genetic loci. The invention relates to murine beta c and beta e polypeptides and the genes encoding them. Disorders of cell growth or differentiation (or susceptibility to

sequence 10708 BP; 2651 A; 2844 C; 2607 G; 2546 T; 60 other;

뫄 9 Matches 1089; Query Match 443 ACAGACCTCTCCAGCATCAACCAGACCCGGCTCGAGTTCCACTTCTCTGGTAGAATGGCC 502 Local Similarity Conservative 65.8%; 97.0%; 0 Score 1025.4; DB 19; Length 10708; Pred. No. 4e-290; Mismatches 26; Indels 8 Gaps

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몽 Ş Š 2050 AGTGGCATGGAGGTCCGGCAGACCCGCTTCATGTTCTTCGTGCAGTTCCCCCACAATGCC 562

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 09-AUG-1996
                                            AAT11104 standard; cDNA; 2272 BP
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                                                                                                                                               ACCCTTAGCTCTCCCTTAGTCAACTATGTAATCTACTCTGCCTCCCTGACCCTGCCACCG
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       A cDNA library prepared using total RNA from human liver was subjected to PCR amplification using primers corresp. to conserved regions within the TGF-beta family. Amplification products were subcloned and sequenced; one clone (designated pSK-MP121) was found to contain a new sequence. Part of the insert from this clone was used to re-screen the human liver cDNA library and a 2272 bp fragment (i.e. the present sequence) coding for a TGF-beta-like protein was isolated. The protein encoded by the cDNA insert has mitogenic and differentiation-inducing properties making it or fusion proteins comprising it or heterodimers of the protein with a cystine knot mottlf protein) useful for inducing tissue regeneration.
264 TGGCCAAGAGAAGCATCTTGGACAAGCTGCACCTGACCGAGCGCCCAACACTGAACCGCC
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2272 BP; 510 A; 663 C; 513 G; 586 T; 0 other;
                                                                                                                                            144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 10; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding transforming growth factor beta MP-121 - has mitogenic and differentiation-inducing activity, e.g. for use in wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR89729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-050788/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bechtold R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JAN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                               84 CTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC
                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-beta; MP-121; mitogen; differentiation; induction; promotion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transforming growth factor beta MP-121 cDNA
                                                                                                                                                                                                                                                               24 CACACTTCTTCCAGGGCGTCTGGCAGCAGGACAGAGTTGAGACCACAGCTGTTGAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maintenance; morphogen;
                                                                                                                                                                                                                                                                                 28 CACATTCCTCCCAGGGTCCCTGGTGCCCAGGACAGAGTTGA-AGCACTCCCGGTTGAGACC
                                                                                                                                                                                                                                                                                                                                                           Loca
                            TGGCCAAGAAAAGTATCCTGGACAAGCTGCACCTCAGCCAGGCGCCCATACTCAGTCGGC 326
                                                               GTCCAGCATGTGGGGGGGCCCACCTTGGAACTGGAGAGCCAGCGGGAGCTGCTTCTTGATC
                                                                                             GCCCAGCATGTTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGAGCTGCTTCTCGATT 266
                                                                                                                                TTCTGGCCTTTCTCCTCCTGGCTCCAACCACAGTGGCCACTCCCAGAGCTGGCGGTCAGT
                                                                                                                                                              TCCTGGCTCTTCTGTTCCTGACTCCAACCACAGTAGTGAACCCCAAAAACTGAGGGTCCAT
                                                                                                                                                                                                                             CTGAATATAGGCTTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTTGC
                                                                                                                                                                                                                                                                                                                                          958;
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neidhardt H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95DE-1011243
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                                                                                                                                                                                                                                                                                                                                            50.0%; Score 779.4; DB 17; Length 2272; 79.8%; Pred. No. 3.2e-218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pohl J, Hoetten
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28 CACATTCCTCCCAGGGTCCCTGGTGCCCAGGACAGAGTTGA-AGCACTCCCGTTGAGACC

Query Match 49.9%; Best Local Similarity 79.6%;

Sequence 2272 BP; 510 A; 663 C; 511 G; 585 T; 3 other;

Matches 956;

Conservative

0;

Score 778; DB 22 Pred. No. 8.3e-21 Mismatches 238;

DB 22;

Length 2272; Indels

7;

Gaps

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                08-MAY-2001
                                                      AAF74421;
                                                                                        AAF74421 standard; DNA; 2272 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAGACCATGAATATAAGAGTTCTTGTGCTAAGACCATATGACACCAACCTCACCTTGA 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTCAAGCTGCCTGCAGCCAGGGGCACCTGACCCTGGAGCTGGTACTTGAAGGCCAGG 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCAGTGCCCACTACACATAG 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATCCAGCCTGAAGGCTATGCCATGAACTTCTGCACTGGGCCAGTGCCCACTACATGTGG 983
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                                                                                                                                                                                                                                                        TGGTCGAGGCCTGCGGGTGTAGTTAGCTTATGGGTGATACAGGCTGCCTGAGGTAGAATG
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                                                                                                                                                                                    G 1221
                                                                                                                                                                                                                                                                                                                                TGTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGACTGACATACCTGACATAG
                                                                                                                                                                                                                                                                                                                                                                  TGTCTTTGCTCTACTATGACAGGGACAGCAACATTGTCAAGACGGATATACCTGACATGG 1163
                                                                                                                                                                                                                                                                                                                                                                                                        ACACAGCTGCAGGCACCACTGGAGGGGGCTCATGCTGTGTACCCACGGCCCCGGCGCCCCC 1100
                  (first entry)
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Human; transforming growth factor-beta; monomeric protein; MP52; MP121; dimeric protein; TGF-beta; vulnerary; antiulcer; nootropic; neuroprotective; antiinfertility; osteopathic; gene therapy; bone; cartilage; dental; wound healing; connective tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TGF-beta MP121 nucleotide sequence SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a protein (I) selected from the members of the transforming growth factor-beta (TGF-beta) superfamily, which is monomeric due to substitution or deletion of a cysteine which is responsible for dimer formation. Also described are: (I) nucleic acid (II) encoding (I); (2) expression vector (III) containing (II) in a suitable vector system; (3) host cell (IV) containing (II) capable of producing (I); and (4) a pharmaceutical composition (V) containing (I), (II) or (IV). (I) has vulnerary, antiulcer, nootropic, neuroprotective, antiinferfility and osteopathic activities, and can be used in gene therapy. (V) is useful for the prevention or therapy of diseases for which also the dimeric form of the protein would be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel monomeric protein of transforming growth factor-beta family for prevention or therapy of diseases associated with bone, cartilage damage, promotion of wound healing, has substitution or deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-228100/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 17-20; 31pp; English.
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                                                                            tissue regeneration, angiogenesis, wound healing including ulcers, burns, injuries or skin grafts, induction of proliferation of progenitor cells or bone marrow cells, for maintenance of a state of proliferation or differentiation, for treatment or preservation of tissue or cells for organ or tissue transplantation, for integrity of gastrointestinal lining and for treatment of disturbances in fertility, contraception or
                                                                                                                                                                                                                                                                                                                         indicated. Diseases treatable include diseases associated with bone and/or cartilage damage or affecting bone and/or cartilage disease or situations in which cartilage and/or bone growth is desirable, for spinal fusion, for damaged or diseased tissue associated with connective tissue
                                                                                                                                                                                                               situations, tissue of the sensory system, liver, pancreas, cardiac, blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane, endothelium, epithelium, for promotion or induction of nerve growth,
                                                                                                                                                                                                                                                                            including tendon and/or ligament, periodontal or dental tissue including dental implants, neural tissue including CNS tissue and neuropathological
                                          rGF-beta monomeric protein MP121, from the present invention.
                                                                pregnancy.
                                                              The present sequence encodes the specifically claimed
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                                                                 ACACAGCTGCAGGCACCACTGGAGGGGGCTCANNNTGTGTACCCACGGCCCGGCGCCCCCC
                                                                                                                                CAGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCTCAATCTTCTCAAGGCCA
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                                                                                                                                                                                                                                TCATCCAGCCTGAAGGCTATGCCATGAACTTCTGCACTGGGCAGTGCCCCACTACATGTGG 983
                                                                                                                                                                                                                                                                CTACTCAGTACCTGCTGGAGGTGGATGCCAGTGGCTGGCATCAACTCCCCCTAGGGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCAGCATGTTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGGAGCTGCTTCTCGATT 266
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Matches Query Match

Local Similarity les 232; Conserv

Conservative

Mismatches

33; Indels

0; Gaps

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Score 212.2; DB 14; Length 265; Pred. No. 4e-52;

13.6%; 87.5%;

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925 CATCCAGCCTGAAGGCTATGCCATGAACTTCTGCACTGGGCAGTGCCCACCTACATGTGGC 984

CATCCAGCCTGAGGGCTACGCCATGAACTTCTGCATAGGGCAGTGCCCACTACACATAGC

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AAQ47710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
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                                The sequences given in AAQ47709-10 represent embryo and liver derived human transforming growth factor-beta (TGF-beta) genes repectively. The proteins encoded by these sequences may be used in a pharmaccutical composition for the treatment of various bone, cartilage or tooth defects and in tissue and wound repair processes. These proteins may also be used as immunosuppressors in organ transplants and in cosmetic surgery. Antibodies raised against these proteins may be
                            cosmetic surgery. Antibodies used for diagnostic purposes.
Sequence 265 BP; 58 A; 80 C; 69 G; 58 T; 0 other;
                                                                                                                                                     Claim 4; Page 18; 29pp; English.
                                                                                                                                                                          New transforming growth factor-beta family proteins and DNA - used in tissue and wound repair, in treatment of bone, cartilage and tooth defects, and antibodies for diagnosis
                                                                                                                                                                                                                                                      WPI; 1993-272824/34.
                                                                                                                                                                                                                                            P-PSDB; AAR45447
                                                                                                                                                                                                                                                                                    Hoetten G,
                                                                                                                                                                                                                                                                                                        (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL
                                                                                                                                                                                                                                                                                                                                         12-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                          W09316099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organ transplant; cosmetic surgery; antibody; diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ47710 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-beta-like clone MP-121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1221 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone; cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1224 G 1224
                                                                                                                                                                                                                                                                                  Neidhardt H;
                                                                                                                                                                                                                                                                                                                                       92EP-0102324
                                                                                                                                                                                                                                                                                                                                                                 93WO-EP00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 2..265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tooth; wound repair; immunosuppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropolesis; haemophilia; cystic fibrosis; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of the genomic region between murine activin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV38239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV38239 standard; DNA; 5099 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liver activin; beta c; beta e; cell differentiation; haematopolesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopolesis, particularly erythropolesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09822492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                menstrual disorder; transgenic; modulator; ss.
                                                                                                                                                                                                                                                                 are diagnosed by measuring liver activin gene activity or by detecting mutation in the liver activin gene. Disorders of haematopoiesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin
                                                                                                                                                                                                                                                                                                                                              murine liver activin beta c and beta e genes. The invention relates to murine beta c and beta e polypeptides and the genes encoding them. Disorders of cell growth or differentiation (or susceptibility to them)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AGTAGAGGCCTGTGGGTGCAGTTAG 265
                                                                                                                                                                                                                                                                                                                                                                                                             This represents the nucleotide sequence of the genomic region between
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4B-C; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating liver, bone and haematopoietic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding sub-units of liver activin useful for regulating growth and differentiation of cells, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-312408/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonadio J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCAGCTGCTGGCACCACTGGCAGGGGCTCGTGCTGCGTGCCTACATCTCGGCGCCCCTCT 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGACTGACATACCTGACATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTTTGCTCTACTATGACAGGGACAGCAACATTGTCAAGACGGATATACCTGACATGGT 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCGAGGCCTGCGGGTGTAGTTAG 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fang J;
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  PT DR XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or the transgenic animals, are useful for screening for liver activin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5099 BP; 1305 A; 1425 C; 1154 G; 1215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1375 TTGACCCAGTACACCCATCCTCAGCCTTAAGTTAGAGGCTAATCGACTCCTACATATA-- 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liver activin; beta c; beta e; cell differentiation; haematopolesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteopolesis; haemophilia; cystic fibrosis; immunoass;
                                                                                                                                                                                                                                                                                                                                                         Murine liver activin beta e polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                     AAV38238;
                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        AAV38238 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CAATGTCATTTTGTTCCTGGCAAACACACCCTTAGCTCTCCCTTAGTCAACTATGTAATC
                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                             menstrual disorder; transgenic; modulator; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                      28-MAY-1998
                                                                                                                                                         WO9822492-A1
New isolated nucleic acid encoding sub-units of liver activin
                                                                                             20-NOV-1996;
                                                                                                                  20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                      P-PSDB; AAW60618.
                                  WPI; 1998-312408/27.
                                                     Bonadio J,
                                                                       (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACTCTGCCTCCCTGACCCTGCCACCGGAAGGTTCCTATTCCACGATGATATGCCTTAGT 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTCCCCTT 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TATGTCATTTTGTCCTAG---CAAACACCCCTTAGCTCCCCTTAGTCAACTATGTAATC 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTCCCCTT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                     Fang J;
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                              96US-0752919
                                                                                                                    97WO-US20882
                                                                                                                                                                                        /*tag= b
279..1265
                                                                                                                                                                                                              216..278
                                                                                                                                                                                                                                           Location/Qualifiers 216..1268
                                                                                                                                                                                                                     /product-
                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                   /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                         polypeptide"
                                                                                                                                                                                                                                                                                                          cystic fibrosis; immunoassay:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7:
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RESULT 8
AAQ10891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                              Encodes Xenopus Bone Morphogenetic Factor M3
                                                                                                                     13-MAY-1991 (first entry)
                                                                                                                                                                                                                                           AAQ10891 standard; DNA; 687 BP
                                                                                                                                                                                                                                                                                                                                                                                               1262 CAGCTAGCAACAGGG 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1183 TAGTTAGCTTATGGG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         968 CCACTATGTAGACTTCCAGGAGCTGGGGTGGCGGGATTGGATCCTGCAGCCGGAGGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883 GTTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908 TCGGGCCAGGAGGACTCCCACCTGTGAGCCTGAGACCCCCTTATGTTGTAGGCGAGA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   823 TCGGGTTCGCCGGCGAGGTATCGATTGCCAGGGGGGGGTCCAGGATGTGCTGTCGACAAGA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders {\bf r}_{\rm c}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATAATGGCAATGTGGTCAAGACCGATGTGCCAGACATGGTAGTAGAGGCCTGTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGGACAGCAACATTGTCAAGACGGATATACCTGACATGGTGGTCGAGGCCTGCGGGTG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCAGGGGCTCCTGCCTGCCTACATCTCGGCGCCCCTCTGTGTTTTGCTCTACTATGA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCAC 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; F19 2; 141pp; English.
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Similarity 63.7%; Pred. No. 6e-32;
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                                        1192 TATGGGTGATA 1202
                                                                                                                                                                                                                        1072 CTCGTGCTGCGTGCCTACATCTCGGCGCCCTCTGTCTTTGCTCTACTATGACAGGGACAG 113:
                                                                                                                                                                                                                                                                                                                                                 1012 TCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCTGGTGGCACCACTGGCAGGGG 107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Xenopus laevis liver-derived DNA library in Charon 28 vector, was screened with a rat activin beta-A cDNA probe. Five clones were isolated, including clone M3. They were subcloned in pUC19 and used to transform competent E.coli HB101 cells. Transformant E.coli HB101/pXar3 coding for the M3 BNP was sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 687 BP; 210 A; 145 C; 149 G; 179 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                            247 TTATTGCATGGGCCTTTGCCCAATGCATATCCCTGGAGCCCCAGGTACGGGAGGCTCATT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    952 CTTCTGCACTGGGCAGTGCCCACTACATGTGGCAGGCATGCCTGGCATCTCTGCCTCCTT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         892 AGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTATGCCATGAA 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 AAAGAGAAGTCTTAACTGTGATCAGAACTCCAATCTGTGCTGTAGGAAAGACTATTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832 CCGGCGAGGTATCGATTGCCAGGGGGGGTCCAGGATGTGCTGTCGACAAGAGTTTTTTTGT 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     775 TTCCCACAGGCCTTTTGTGGCAGCCCAGGTAAGGGT---TGAGGGCAAGCATCGGGTTCG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAQ10890 and AAQ10892-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 2; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis bone morphogenetic protein and DNA encoding used in therapy of fracture or osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR10991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-075112/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakami K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEMICAL IND KK. (SCIT-) SCITECH RESEARCH CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP416578-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMF; osteoporosis; fracture; cartilage; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 TTCCCACCAGCCATTTCTGGTAGCACAGGCCAAAGTCCATGAACAAAGTCACCATGCTAC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                 CCACACCACGGTATTAAATCTCATTAAGGCCAAC----AATATCCAGACAGCAGTGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACTTCAAGGATATTGGGTGGAATGATTGGATTATAAAACCAGAGGGATATCAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%;
Similarity 61.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90JP-0190774.
89JP-0229250
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2..478
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0;

Score 143.4; Pred. No. 1e Mismatches

1e-31;

DB 12; Length 687; 156; Indels

9; Gaps

246

XSXFXBX

В 9 8 ş В Ş Dδ õ В ş В Ş ₽ Ş

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AAK94607 RESULT 9

AAK94607 standard; cDNA; 1616 BP.

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                                                                                                                                                                                                                                                                                                                                  molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed and constitutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1999; 99JP-0194486
11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human full-length cDNA, SEQ ID NO: 3557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830 primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                           Sequence 1616 BP; 352 A; 480 C; 449 G; 335 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO, 3557; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                          specification, but was obtained in CD-ROM format directly from EPO
1004 GCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCACT 1063
                                884 TTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTAT 943
                                                                                                                                                           913 CGGGCCAGGAGGAGCCCCCACCTGTGAGCCTGCGACCCCCTTATGTTGCAGGCGAGAC 972
                                                                                                                                                                             824 CGGGTTCGCCGGCGAGGTATCGATTGCCAGGGGGGGTCCAGGATGTGCCTGTCGACAAGAG 883
                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-524255/58.
                                                                                             231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa T, Isogai T, Hayashi K, Is
su A, Sugiyama T, Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM93672
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                            8.8%;
62,9%;
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                            Score 137; DB 22; Length 1616; Pred. No. 1.2e-29;
                                                                                                                                                                                                                              Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otsuki T,
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koga H;
                                                                                                                                                                                                                              6
                                                                                                                                                                                                                              Gaps
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Query Match Best Local Similarity

8.8%;

Score 137; DB 17; Pred. No. 1.4e-29;

Length 2419;

Sequence 2419 BP; 557 A; 648 C; 661 G; 553 T; 0 other;

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RESULT 10
AAT16883
ID AAT16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human growth differentiation factor-12 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT16883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1267 AGCTAGC 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1184 AGTTAGC 1190
                                      A cDNA clone (AAT16883) codes for human growth differentiation factor-12 (GDF-12 - AAR92754), a new member of the transforming growth factor beta superfamily that is expressed specifically in liver. It was obtd. from an adult liver cDNA library in lambda ZAP II using a GDF-12 probe obtd. by PCR amplification (see also AAT16884-93) of mouse cDNA. The isolated sequence can be incorporated into a vector and used for prodn. of recombinant GDF-12 in transformed host cells or used to design GDF-12 antisense polynocleotides useful for treating cell proliferative disorders associated with GDF-12 expression, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell proliferation; cancer; diagnosis; gene therapy; antisense; transforming growth factor beta; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth differentiation factor-12; GDF-12; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT16883 standard; cDNA; 2419 BP
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                                                                                                                                                                                                             and therapeutic methods esp. in methods for treating a cell proliferative disorder of liver origin
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9602559-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                  Claim 3; Page 40-43; 52pp; English.
                                                                                                                                                                                                                                     DNA encoding Growth Differentiation Factor-12 - used in diagnostic
                                                                                                                                                                                                                                                                   P-PSDB; AAR92754.
                                                                                                                                                                                                                                                                                    WPI; 1996-105850/11.
                                                                                                                                                                                                                                                                                                            Esquela AF,
                                                                                                                                                                                                                                                                                                                                                                    26-SEP-1994;
13-JUL-1994;
                                                                                                                                                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-1995;
                            in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGC 1266
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                                                                                                                                                                                                                                                                                                                Lee S;
                                                                                                                                                                                                                                                                                                                                                                     94US-0274215
                                                                                                                                                                                                                                                                                                                                                                                     9405-0311370
                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US08745
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AAV38240
ID AAV3
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          P-PSDB; AAW60619.
                      HPI;
                                          Bonadio J,
                                                              (UNMI ) UNIV MICHIGAN
                                                                                      20-NOV-1996;
                                                                                                           20-NOV-1997;
                                                                                                                                   28-MAY-1998.
                                                                                                                                                        W09822492-A1
                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                  menstrual disorder; transgenic; modulator; human; ss.
                                                                                                                                                                                                                                                                                                           Liver activin; beta c; beta e; cell differentiation; haematopoiesis; erythroid; ovarian follicular maturation; hormone; neuronal survival spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoas
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Human liver activin beta e polypeptide encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                    AAV38240;
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                    1998-312408/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGACAGCAACATTGTCAAGACGGATATACCTGACATGGTGGTCGAGGCCTGCGGGGTGT 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCT----TGGCCT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCACT 1063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231;
                                         Fang J;
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                      96US-0752919
                                                                                                           97WO-US20882
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127..1126
                                                                                                                                                                                                                                                Location/Qualifiers
77...1120
                                                                                                                                                                          /*tag-
                                                                                                                                                                                                            /product= "activin beta e polypeptide" 77..126
                                                                                                                                                                                                                                   /*tag-
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XXX

AAN70316;

09-APR-1991 (first entry)

Sequence encoding human inhibin beta-chain precursor beta-B

RESULT 12 AAN70316

AAN70316 standard; cDNA; 1966 BP

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Best Local Similarity 62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating expthropoiesis or osteomalacia) or haematopoiesis, particularly erythropoiesis for treating hematopoiesis, particularly expthropoiesis for treating hematopoiesis, to generate antidisorders. Antibodies are useful in immunoassays, to generate antidiotypic antibodies (which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, or the transgenic animals, are useful for screening for liver activin modulators.
  1124
                                                                                                                                       1124
                                         1184 AGTTAGC 1190
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                                                                                                                                                                                                                                                                                                                        1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This cDNA encodes a human liver activin beta e polypeptide. The invention provides murine liver activin beta c and beta e genes. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the activin gene. Disorders of haematopoiesis, crythroid differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ovarian follicular maturation, hormone secretion, neuronal
                                                                                                                                                                                                                                                                                                                                                                       990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding sub-units of liver activin useful for regulating growth and differentiation of cells, e.g.
                                                                                                                                                                                                                                                                            950
                                                                                                                                                                                                                                                                                                                                                                                                   830 CATTACGTAGACTTCCAGGAACTGGGATGGCGGGACTGGATACTGCAGCCCGAGGGGTAC 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              884 TTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTAT 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        824 CGGGTTCGCCGGCGAGGTATCGATTGCCAGGGGGGGGTCCAGGATGTGCTGTCGACAAGAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating liver, bone and haematopoietic disorders
                                                                               CATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGC
                                                                                                    AGGGACAGCAACATTGTCAAGACGGATATACCTGACATGGTGGTCGAGGCCTGCGGGTGT 1183
                                                                                                                                                                                                             GGCAGGGGCTCGTGCTGCGTGCCTACATCTCGGCGCCCCTCTGTCTTTGCTCTACTATGAC
AGCTAGC 1130
                                                                                                                                                                          GCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCT-----TGGCCT
                                                                                                                                                                                                                                                                                                          GCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCACT 1063
                                                                                                                                                                                                                                                                                                                                                           CGGGCCAGGAGGAGCCCCCACCTGTGAGCCTGCGACCCCCTTATGTTGCAGGCGAGAC 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 135.4; DB 1
Pred. No. 3.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-1986;
03-OCT-1985;
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1966 BP; 424 A; 557 C; 621 G; 364 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulating clinical condition or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1987-137512/20.
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920
                                                                                                                                                                                                                                        803
                                                                                                                                                                                                                                                                   618 GTGGTGCCGGTGTTCGTGGACCCAGGCGAAGAGTCGCACCGGCCCTTTGTGGTGGTGCAG 677
                                                                                                                                                                                                                                                                                      743 GTGGCCACAGTTCCTTGATCCTGGGCTGGTTTTCCCACAGGCCTTTTGTGGCAGCCCAG 802
                                                                                                                                                  738
                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                            GTGGCAGGCATGCCTGGCATCTCTGCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAA 1039
                                                                                                                                                                                                                                       GTAAG----GGTTGAGGGCAAGCATCGGGTTCGCCGGCGAGGTATCGATTGCCAGGGGGGG 859
                                                                                       TGGATCATAGCACCCACCGGCTACTACGGGGAACTACTGTGAGGGGAGCTGCCCAGCCTAC 857
                                                                                                                     TGGATCATCCAGCCTGAAGGCTATGCCATGAACTTCTGCACTGGGCAGTGCCCACTACAT 979
                                                                                                                                                  ACCAACCTCTGTTGCAGGCAACAGTTCTTCATTGACTTCCGCCTCATCGGCTGGAACGAC
                                                                                                                                                                             TCCAGGATGTGCTGTCGACAAGAGTTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGAC 919
                                                                                                                                                                                                             GCTCGCCTGGCCACAGCAGCCACCGCATTCGCAAGCGAGGCCTGGAGTGCGATGGCCGG
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85US-0783910.
86US-0827710.
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/*tag- b
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                                                                                                                                                                                                                                                                                                                                             8.3%;
                                                                                                                                                                                                                                                                                                                                             Score 129.4; DB 8; Length 1966; Pred. No. 2.2e-27;
                                                                                                                                                                                                                                                                                                                                Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 CCTCTGTCTTTGCTCTACTATGACAGGGACAGCAACATTGTCAAGACGGATATACCTGAC 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN70318 standard; cDNA; 1530 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence encoding porcine inhibin beta-chain precursor beta-B.
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                                                       biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed
                                                                                                                                        A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin alpha or an inhibin beta
                                                                                                                                                                                                                                          Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        915
                                        at modulating the climical condt. or reproductive physiology of
                                                                                 chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or
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                                                                                                                                                                                                                                                                                                                                  Mason AJ,
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03-OCT-1985;
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 Sequence 1530 BP; 318 A; 469 C; 511 G; 232 T; 0 other;
                                                                                                                                                                                                Disclosure; Fig 1B; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scrofa domestica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTGGTCGAGGCCTGCGGGTG 1182
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85US-0783910.
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Query Match Best Local Similarity Matches 251; Conserv

Conservative

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7.8%; 56.2%;

Score 121; DB 8; Pred. No. 5.7e-25; Mismatches 190;

Length 1530; Indels

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RESULT 14
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P-PSDB; AAP70200
          WPI; 1987-137512/20.
                                   Mason AJ,
                                                                                               12-SEP-1986;
03-OCT-1985;
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                                                           (GETH ) GENENTECH INC.
                                                                                     10-FEB-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   904 CGCATGCGGGGCCTGAACCCGTTCGGCACAGTGAACTCCTGCTGCATCCCCACCAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACATGGTGGTCGAGGCCTGCGGGTGT 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGACCAACCTCTGTTGCAGGCAACAGTTCTTCATCGACTTCCGCCTCATTGGCTGGAGT
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                                Seeburg PH
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85US-0783910
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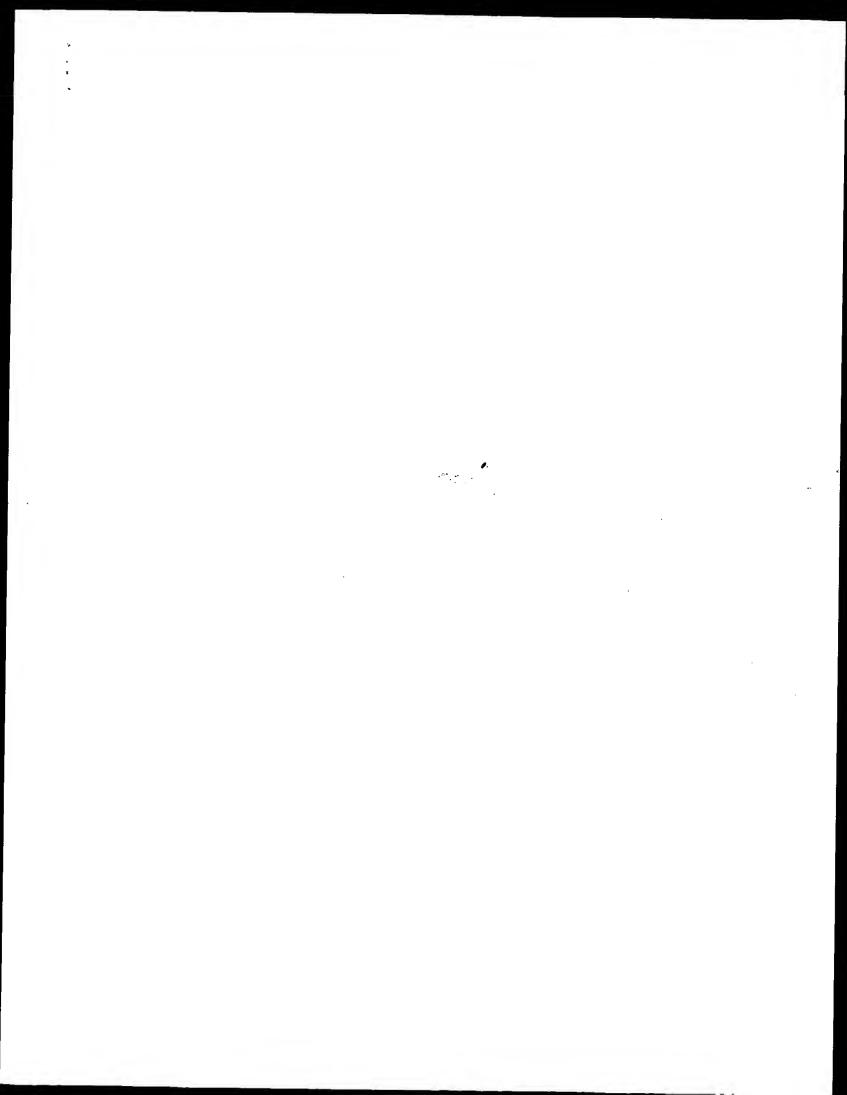
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                                                                                           Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                      Human pancreas cell specific cDNA sequence SEQ ID NO:370.
                                                                                    neuroprotective;
                                                                                                                                                                                                                  10-SEP-2001
                                                                                                                                                                                                                                                     AAH57530;
                                                                                                                                                                                                                                                                                    AAH57530 standard; cDNA; 1620
                                                                                                                                                                                                                                                                                                                                                                                 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1112 CTCTACTATGACAGGGACAGGAACATTGTCAAGACGGATATAACCTGACATGGTGGTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            processing in transformant cell culture or in experiments waste at modulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      992 CCTGGCATCTCTGCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCT 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1B; 48pp; English.
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Pred. No. 1.3e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for dispossis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sornasse T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1099 TGCAGGCCCGGCAGTCTGAAGACCACCCTCATCGCCGGCGTCGGCGGGGCTTGGAGTGTG 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 287-288; 327pp; English.
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                                                                                         1399 AGCTGAGACCCATGTCCATGTTGTACTATGATGATGGTCAAAACATCATCAAAAAGGACA 1458
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                                             1152 TACCTGACATGGTGGTCGAGGCCTGCGGGTGTAGTTAG 1189
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  TTCAGAACATGATCGTGGAGGAGTGTGGGTGCTCATAG 1496
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Search completed: October 11, 2002, 22:14:58 Job time: 204.733 secs



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US-08-455-550-2
US-08-765-662-13
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US-08-197-792-44
US-08-459-850-44
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Query Match Best Local Similarity 100.0%;	RESULT 1 US-08-482-577B-3 Sequence 3, Application US/08482577B Patent No. 5807713 GENERAL INFORMATION: APPLICANT: HCTTEN, GERTRUD APPLICANT: BECHTOLD, ROLF APPLICANT: BECHTOLD, ROLF TITLE OF INVENTION: GROWTH/DIFFE INVERSIBE: MIKAIDO, MARMELSTEI ADDRESSEE: SUITE 330 CITY: WASHINGTON STREET: SUITE 330 CITY: WASHINGTON STATE: DC COUNTRY: USA ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DC SOFTWARE: PatentIn Release #1. CURRENT APPLICATION UNMBER: US/08/482. FILING DATE: NAME: KLESNER, SHARON REGISTRATION NUMBER: 9564* TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-4810 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1558 base pairs TYPE: DNA DUBLICATION INFORMATION: TELEPHONE: 202/638-4810 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1558 base pairs TYPE: DNA DUBLICATION INFORMATION: DOCUMENT NUMBER: US/08/289, 22: FILING DATE: 11-ear MOLECULE TYPE: DNA DUBLICATION INFORMATION: DOCUMENT NUMBER: US/08/289, 22: FILING DATE: 12-AUG-1994	28 93.4 6.0 1667 1 U. 29 70.4 4.5 926 1 U. 30 70.4 4.5 926 3 U. 31 70.4 4.5 926 5 P. 32 70.4 4.5 1345 3 U. 33 70.4 4.5 1345 3 U. 34 70.4 4.5 1345 4 U. 35 70.4 4.5 1345 5 P. 36 68.2 4.4 420 1 U. 38 68.2 4.4 420 5 P. 40 68.2 4.4 1003 2 U. 41 68.2 4.4 1003 2 U. 42 68.2 4.4 1723 1 U. 43 68.2 4.4 1723 1 U. 45 68.2 4.4 1723 1 U.
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1558; No. 0;	Vers	US-08-455-550-1 US-08-352-670B-1 US-08-333-576C-1 US-08-80B-324-1 US-08-80B-324-1 US-08-93-576C-3 US-08-93-576C-3 US-08-93-576C-3 US-08-9149-11 US-08-741-589A-11 US-08-741-589A-11 US-08-741-589A-11 US-07-807-364B-13 US-08-469-411-11 US-08-469-411-11 US-08-469-411-11 US-08-469-411-11 US-08-469-411-11 US-07-801-703-10 US-07-901-703-10 US-08-147-023-28
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Matches 1558;
   AGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCACTGGCAGGGGCTCGTGCTG 1080
                        AGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCACTGGCAGGGGGTCCGTGCTG 1080
                                                                                            TGGGCAGTGCCCACTACATGTGGCAGGCATGCCTGGCATCTCTGCCTCCTTTCACACTGC 1020
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US-09-218-176-3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT//
ETLING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT//
                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE TITLE OF INVENTION: TGF- FAMILY NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth Street, N. W., G Street Lobby, STREET: Suite 330

CITY: Washington

STATE: DC
                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6:
FILING DATE: 12-JUL-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: H TTEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, ROLf
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 01-JUL-1994
PRIOR APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTONNEY/ACENT INFORMATION:
NAME: KITTS, MONICA Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1558 base pairs
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Best Local Similarity
Matches 1558; Conserv
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CGTGCAGTTCCCCCACAATGCCACCCAGACCATGAATATAAGAGTTCTTGTGCTAAGACC
           CGTGCAGTTCCCCCACAATGCCACCCAGACCATGAATATAAGAGTTCTTGTGCTAAGACC
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RESULT 3 US-08-482-577B-1

Sequence 1, Application US/08482577B Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD APPLICANT: NEIDHARDT, HELGE APPLICANT: BECHTOLD, ROLF

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                                           TTTGTCCTAGCAAACACCCCTTAGCTCCCCTTAGTCAACTATGTAATCTACTCTGCCTCC 1500
                                                                      TCCAGAATGGAAACACCTTTCTAAGCATGCAGACATCCCTCTGTGGACTTCAGGGGATCC
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CTGACCCTGCCACCGGAAGGTTCCTATTCCACGATGATATGCCTTAGTGTCTCCCCTT
                                  TTTGTCCTAGCAAACACCCCTTAGCTCCCCTTAGTCAACTATGTAATCTACTCTGCCTCC
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Best Local (
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 2272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA SEQUENCES ENCODING TITLE OF INVENTION: GROWTH/DIFFERENTIATION NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: KLESNER, SHARON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
 441, GCCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTTCTCCTCTGATAGAACTGCTG 500
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 CACACTTCTTCCAGGGCCTCTGGCAGCCCAGGACAGAGTTGAGACCACAGCTGTTGAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/482,577B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 50.1%; Local Similarity 79.9%;
                                                                                       CCCTGTTGGAGCATGACCAGAGACAAGAAGAATATGAGATCATCAGCTTTTGCTGACACAG 446
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                                    ACCTCTCCAGCATCAACCAGACCCGGCTCGAGTTCCACTT---CTCTGGTAGAATGGCCA 503
                                                                       CACTTCTAGAG - - - GACAACAGGGAACAGGAATGTGAAATCATCAGCTTTGCTGAGACAG
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Pred. No. 3.4e-229;
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HOTTEN
APPLICANT: NEIDHARI
APPLICANT: BECHTOLL
APPLICANT: POHL, JE
                                                                                                                                                                                                                          Sequence 2, Application US/08289222E Patent No. 6120760
                                                                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO,
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                                                                                                                           TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS TITLE OF INVENTION: FAMILY
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                                      STREET: 655 FIFTEENTH STREET, STREET: SUITE 330 CITY: WASHINGTON
COUNTRY: USA
ZIP: 20005-5701
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                                                                                                                                                                  NEIDHARDT, HELGE
BECHTOLD, ROLF
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                                                                 MARMELSTEIN, MURRAY & ORAM
TH STREET, N. W., G STREET LOBBY
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APPLICATION NUMBER: PCT/EP93/GAPTION PCT/EP93/GAPT/EP93/GAPTION PCT/EP93/GAPTION PCT/EP93/GAPTION PCT
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INFORMATION FOR SEQ ID NO: 2:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/289,222
FILING DATE: 12-AUG-1994
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 07-JUL-1994
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   GCCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTTCTCCTCTGATAGAACTGCTG 500
                                                                                                                                                                       CCCTGTTGGAGCATGACCAGAGACAAGAAGAATATGAGATCATCAGCTTTGCTGACACACAG 446
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                                  ACCTCTCCAGCATCAACCAGACCCGGCTCGAGTTCCACTT---CTCTGGTAGAATGGCCA 503
                                                                                                                                     CACTTCTAGAG - - - GACAACAGGGAACAGGAATGTGAAATCATCAGCTTTGCTGAGACAG
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                                                                                                                                                                                                                                                    RESULT 5
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APPLICANT:
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                                                                                      APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
APPLICANT: NEW GROWTH/DIFFERENTIATION FACTORS
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
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                               Washington
DC
USA
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                                                          655 Fifteenth Street,
                                                                                                                                                            NEIDHARDT, Helge
BECHTOLD, Rolf
                                                                                                                                                                                      H TTEN, Gertrud
                                                          NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
5 Fifteenth Street, N. W., G Street Lobby
                                                            G Street Lobby
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TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 2272 base pairs
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: DE P 44 23 190.3
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327 CAGTGTCCAGAGGGGCTCTCAAGACCGCGCGCGCAGCGCCTCCGCGGGCCTCGACGGGAAA 386
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APPLICATION NUMBER:
FILING DATE: 12-JUL-
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                     Match 50.1%; Local Similarity 79.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                            TETTGGCCTTTCTCCTCCTGGCTCCAACCACAGTGGCCAGACCTGGCAGAGCTGGCGGTCAGT
                                                                                                                                                                                         TCCTGGCTCTTCTGTTCCTGACTCCAACCACAGTAGTGAACCCCAAAACTGAGGGTCCAT 206
                                                                                                                                                                                                                       CTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC 143
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Pred. No. 3.4e-229;
0; Mismatches 235; Indels
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RESULT 6 US-09-054-526B-2

Sequence 2, Application US/09054526B Patent No. 6197550

GENERAL INFORMATION:
APPLICANT: H TTEN
APPLICANT: NEIDHA
APPLICANT: BECHTO
APPLICANT: POHL,

H TTEN, GERTRUD NEIDHARDT, HELGE BECHTOLD, ROLF

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                                                                                                                                 TGTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGACTGACATACCTGACATGG
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                                                                                                                                                                                                                                                                                                          CAGGCATGCCTGGCATCTCTGCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCA
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LENGTH: 2272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 12-AUG-
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STREET:
CITY: W
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                 327
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REFERENCE/DOCKET NUMBER: P564-8005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: KITTS, MONICA CHIN REGISTRATION NUMBER: 36,1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                     28 CACATTCCTCCCAGGGTCCCTGGTGCCCAGGACAGAGTTGA-AGCACTCCCGTTGAGACC 86
                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
                                                 CAGTGTCCAGAGGGGCTCTCAAGACCGCGCGCTGCAGCGCCTCCGCGGGCCCTCGACGGGAAA 386
                                                                                                                  GTCCAGCATGTGGGGGGCCCCACCTTGGAACTGGAGGGGAGCCAGCGGGAGCTGCTTCTTGATC
                                                                                                                                                  GCCCAGCATGTTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGAGCTGCTTCTCGATT 266
                                                                                                                                                                                      TTCTGGCCTTTCTCCTCCTGGCTCCAACCACAGTGGCCACTCCCAGAGCTGGCGGTCAGT
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                                                                                                                                                                                                                                                      CTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC 143
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WASHINGTON
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US-08-289-222E-5

Sequence 5, Application US/08289222E Patent No. 6120760

GENERAL INFORMATION: APPLICANT: HOTTEN

APPLICANT:

APPLICANT: BECHTOLI APPLICANT: POHL, JI TITLE OF INVENTION:

NEIDHARDT, HELG BECHTOLD, ROLF POHL, JENS HOTTEN, GERTRUD

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                                                                                                                                                   TGTCTTTGCTCTACTATGACAGGGACAGCAACATTGTCAAGACGGATATACCTGACATGG
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TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 5:
                                                 1165 GGTCGAGGCCTGCGGGTGTAGTTAG 1189
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EPO SETILING DATE: 12-FEB-1992 PRIOR APPLICATION DATA:
241 AGTAGAGGCCTGTGGGTGCAGTTAG 265
                                                                                                              985 AGGCATGCCTGGCATCTCTGCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAA 1044
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                        61 AGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCTCAATCTTCTCAAGGCCAA 120
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FILING DATE: 07-JUL-1994
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                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/I
FILING DATE: 12-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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655 FIFTEENTH STREET, N. W., G STREET LOBBY,
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                                                                                                                                                                                                                                                                                              Score 212.2; DB 3
Pred. No. 1.7e-55;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P564-9021
                                                                                                                                                                                                                                                                                                                         DB_3; Length 265;
                                                                                                                                                                                                                                                                                              33; Indels
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RESULT 8

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                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT ATTICATION NUMBER: US/09/054,526b
APPLICATION NUMBER: US/09/054,526b
FILING DATE: 03 APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 5, Application US/09054526B Patent No. 6197550
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO:
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TOPOLOGY: lin
MOLECULE TYPE:
                    1105 GTCTTTGCTCTACTATGACAGGGACAGCAACATTGTCAAGACGGATATACCTGACATGGT 1164
                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                       TITLE OF INVENTION: DNA SEQUENCES ENCOURING NUMBER OF INVENTION: GROWTH/DIFFERENTATION FACTORS NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                     985 AGGCATGCCTGGCATCTCTGCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAA 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EPO FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DE P
FILING DATE: 01-JUL-1994
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STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY
STREET: SUITE 330
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                                                                                                                   AGGCATGCCTGGTATTGCTGCCTCCTTTCACACTGCAGTGCTCAATCTTCTCAAGGCCAA 120
232;
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BECHTOLD, ROLF
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                                                                                                                                                                                                                                                        13.6%; Score 212.2; DB 4 87.5%; Pred. No. 1.7e-55; ative 0; Mismatches 33
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                                                                                                                                           PCT/EP93/00350
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181 GTCTCTGCTCTATTATGACAGGGACAGCAACATTGTCAAGACTGACATACCTGACATGGT 240

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; ORIGINAL SOURCE:
US-08-455-550-2
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Best Local Similarity
Matches 266; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/0845550 Patent No. 5670338 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056,564
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/577,892
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elsenstein, Ronald I
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 40302-FWC-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MURAKAMI, KAZUO APPLICANT: UENO, NAOTO APPLICANT: KATO, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AGTAGAGGCCTGTGGGTGCAGTTAG 265
892 AGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTATGCCATGAA 951
                                                                                                                                   775 TTCCCACAGGCCTTTTGTGGCAGCCCAGGTAAGGGT---TGAGGGCAAGCATCGGGTTCG 831
                                                                                 832 CCGGCGAGGTATCGATTGCCAGGGGGGGTCCAGGATGTGCTCTCGACAAGAGTTTTTTGT 891
                                                  127 AAAGAGAAGTCTTAACTGTGATCAGAACTCCAATCTGTGCTGGTAGGAAAGACTATTATGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                 67 TTCCCACCAGCCATTTCTGGTAGCACAGGCCAAAGTCCATGAACAAAGTCACCATGCTAC 126
                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                    Conservative
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31-MAY-1995
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61.7%;
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                                                                                                                                                                                 Score 143.4; DB 1;
Pred. No. 3.3e-34;
0; Mismatches 156;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                   Length 687;
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RESULT 10
US-08-765-662-13
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Patent No. 5929213
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                          HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1132 CAACATTGTCAAGACGGATATACCTGACATGGTGGTCGAGGCCTGCGGGTGTAGTTAGCT 119:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 CCACACCACGGTATTAAATCTCATTAAGGCCAAC-----AATATCCAGACAGCAGTGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 AGACTTCAAGGATATTGGGTGGAATGATTGGATTATAAAACCAGAGGGATATCAGATAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 CTTGGGCTACA 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 CTCATGCTGTGTCCCTACCAAAAGGCGCCCTTTGTCCATGCTTTACTTTGATAGAAATAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haile, Ph.D., Lisa A REGISTRATION NUMBER: 38,347
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ZIP: 92037
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                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
OTHER INFORMATION:
                  NAME/KEY: Coding Sequence LOCATION: 218...1267
                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                               2419 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application PC/TUS9508745
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Haile, Ph.D., Lisa
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                               TELEPHONE: 619-678-5070
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                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92037
OMPUTED -
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             TOPOLOGY:
                          STRANDEDNESS:
                                                                                                                                TELEFAX:
                                                                                                                                                                             NAME: Haile, Ph.D., Lisa A REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/08745 FILING DATE: 12-JUL-1995
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                                                                                                                                             TELEPHONE:
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Local Similarity 62.9%;
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: CA
TYPE:
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                                                                                                                                 619-678-5099
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             linear
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                            single
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US-08-274-215A-11
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: LOCATION: 218...1267
: OTHER INFORMATION:
PCT-US95-08745-13
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GENERAL INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., LISA
                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                             APPLICANT: Lee, Se-Jin
APPLICANT: ESQUELA, AUTOTA F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                 APPLICATION NUMBER: US/08/274,215A
FILING DATE: 13-UUL-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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ORIGINAL SOURCE:
FEATURE:
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                                                                                                                                                                                                                                                                  CITY:
STATE:
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OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows
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Local Similarity 62.9%;
es 231; Conservation
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Pred. No. 6e-32;
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                                                                                                                                                 Version
                                                                                                                                                                                                                                                                                                   Suite 1400
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Patent No. 5929213
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                                                                                                                                                                                                                                                       APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12 NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                              OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       824 CGGGTTCGCCGGCGAGGTATCGATTGCCAGGGGGGGGTCCAGGATGTGCTGTCGACAAGAG 883
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STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                          COMPUTER:
                                                                                                                                                                COUNTRY:
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               APPLICATION NUMBER:
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28-APR-1997
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                 us/08/765,662
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Sequence 11, Application US/09184933; Patent No. 6130050; GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Haile, Ph.D., Lisa A REGISTRATION NUMBER: 38.347 REFERENCE/DOCKET NUMBER: 07.7 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                 APPLICANT: Lee, Se-Jin
APPLICANT: Esquela, Aurora F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                1184 AGTTAG 1189
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                                                                                                                                                                                                                                                                                     355 AGCTAG 360
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                                                                                                                                                                                                                                                                                                                                                                          295 CATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 12-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 8.7%; Score 136; DB 2; Length 360; Local Similarity 62.8%; Pred. No. 4.3e-32; hes 230; Conservative 0; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CATTACGTAGACTTCCAGGAACTGGGATGGCGGGACTGGATACTGCAGCCCGAGGGGGTAC 120
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ADDRESSEE: Fish & Richardson, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCT-----TGGCCT 234
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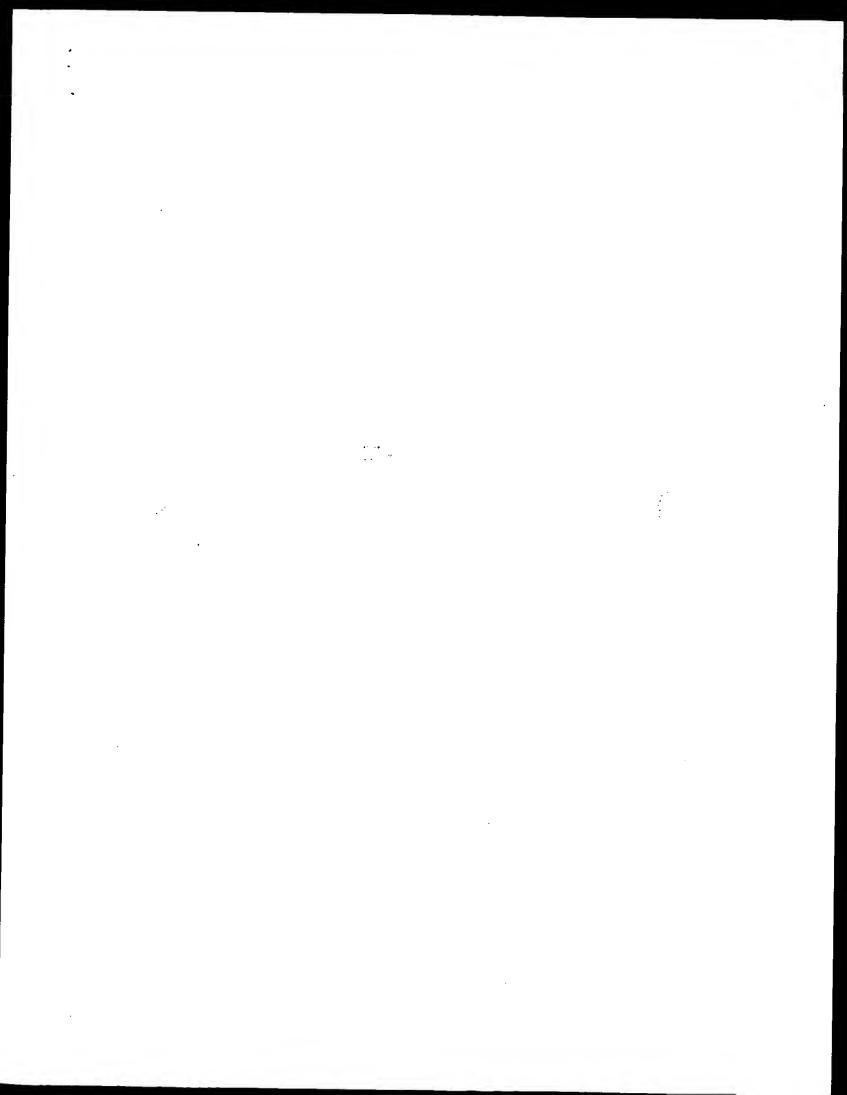
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RESULT 15
PCT-US95-08745-11
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; LOCATION: 1...357
US-09-184-933-11
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     1124 AGGGACAGCAACATTGTCAAGACGGATATACCTGACATGGTGGTGGAGGCCTGCGGGTGT 1183
                                                                                                                                         1184 AGTTAG 1189
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                         181
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APPLICATION NUMBER: 08/2
FILING DATE: 13-JUL-1994
                                                                                                                                                                      295 CATAATGGCAATGTGGTCAAGACGGATGTGGCAGATATGGTGGTGGAGGCCTGTGGCTGC 354
                                                                                                                                                                                                                                                                                                                                                                                  884 TTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTAT 943
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CATTACGTAGACTTCCAGGAACTGGGATGGCGGGACTGGATACTGCAGCCCGAGGGGGTAC 120
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STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGGGCCAGGAGGAGCCCCCACCTGTGAGCCTGCGACCCCCTTATGTTGCAGGCGAGAC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/184,933
                                                                                                       AGCTAG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230; Conservative
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Similarity 62.8%;
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FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...357
                1124 AGGGACAGCAACATTGTCAAGACGGATATACCTGACATGGTGGTGGAGGGCTGGCGGGTGT 1183
                                                                                              1064 GGCAGGGGCTCGTGCTGCGTGCCTACATCTCGGCGCCCTCTGTCTTTGCTCTACTATGAC 1123
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295 CATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGC 354
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ANTI-SENSE: NO
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                                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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NAME: Haile, Ph.D., Lisa
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                                                                                                                                                                                                                                884 TTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTAT 943
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CITY: La Jolla
                                                                                                                                                                                                                                                                61 CATTACCTAGACTTCCAGGAACTGGGATGGCGGGACTGGATACTGCAGCCCGAGGGGTAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,34:
REFERENCE/DOCKET NUMBER: 07
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COMPUTER: IB
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ZIP: 92037
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                                                                GCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCACT 1063
                                                                                                                                 GCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCT----TGGCCT
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Db 355 AGCTAG 360

Search completed: October 11, 2002, 22:15:27 Job time : 47.2042 secs



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                        752.
726.
716.8
714
                     706.6
696
653.8
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509
413.2
299.6
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length: 2000000000
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16707.608 Million cell updates/sec
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1558
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EST: *
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                         AI452079 mm08a04.x
AA242421 mx26a10.r
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BG566943 6Q2589447
                                                                         BC020693 Homo sapi
AA237913 mx14e05.r
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BI246740
BI145698
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                                                                                                                                                                                        BI148079 602912428
BI329959 602980519
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602075120
602023292
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  CH230-23P
602917943
                                                                                                   602026526
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ALIGNMENTS

KEYWORDS SOURCE ORGANISM RESULT 1 BI148079 COMMENT REFERENCE · VERSION ACCESSION DEFINITION FEATURES BASE COUNT TITLE AUTHORS source Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11145 row: g column: 08 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musia; Musiases 1 to 941) 602912428F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5053471 5', mRNA_sequence Unpublished (1999)
Contact: Robert Strausberg, Ph.D. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) EST BI148079.1 GI:14608080 BI148079 house mouse High quality sequence stop: 887 202 /Strain="taxon:10090"
//Bb_xref="taxon:10090"
//Clone="IMAGE:5053471"
//Clone="IMAGE:5053471"
//Clone="INTAGE:5053471"
//Lab_host="ADH10B (Ti phage-resistant)"
//Lab_host="DH10B (Ti phage-resistant)"
//Lab_ /strain-"FVB/N" /organism="Mus musculus" ocation/Qualifiers . 941

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 95.1%;
                                                                                                                                                        CTACATATATGTCATTTTGTCCTAGCAAACACCCCTTAG-CTCCCCTTAGTCAACTA- 1481
                            TGCCTTAGTGTCTCCCCTT 1558
TGCCTTAGTGGTTTCCCCT 917
                                                       TGTAATCTACTCTGGCTCCCTTGACCCTGCAGCGGAAGGGTTCCTATTCCAACGATGATA
                                                                                                                        CCACAAGCAATGTCATTTTGTTCCTAGCAAAAAACCCTTAGTCTCCCTTTAGTCAACTAT 838
                                                                                       TGTAATCTACTCTGCCTCCC-TGACCCTGCCACCGGAAGGTTCCTATTCC-ACGATGATA 1539
                                                                                                                                                                                          GACATGGTTGACCCAGTACAACCATCCTCAGGCTTAAGTTAGAGGCTAATCGATGGCCTA 778
                                                                                                                                                                                                                                                                            GTTCCCACTTCTGTCCAGAATGGAAACACCTTTCTAAGCATGCAGACACCCTCTGTGGA 1307
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                                                                                                                                                                                                                                                                                                                                                                                         GCTTATGGGTGATACAGGCTGCCTGAGGTAGAATGGCCTTCCTCAGGAAGGGGAAACTCT 598
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TITLE
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                                                                                                                 TCAGCCAGCGCCCCATACTCAGTCGGCCAGTGTCCAGAGGGGGCTCTCAAGACCGCGCTGC
                                                                                                                                                  TCAGCCAGCCCCCATACTCAGTCGGCCAGTGTCCAGAGGGGCTCTCAAGACCGCGCTGC
                                                                                                                                                                                                                 AGAGCCAGCGGGAGCTTCTCGATTTGGCCAAGAAAAGTATCCTGGACAAGCTGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11327 row: f column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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602980519F1 NCI_CGAP_Li9 Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5133317"
/clone=lib="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 246 c 217 g 179 t
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Pred. No. 8.1e-192;
0; Mismatches 14;
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SOURCE
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Tissue Procurement: Jeffrey E. Green, M.D.
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National Institutes of Health,
Unpublished (1999)
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                                                              /clone="IMAGE:5125287"
/clone="NCI_CGAP_L19"
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/lab_host="DH10B (T1 phage resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Site_2: Sali; Cloned unidirectionally. Primer: Oliverage insert size 19 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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mRNA sequence. BI145698 BI145698.1 GI

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602909844F1 NCI_CGAP_Li9

841 bp mRt Mus musculus

mRNA Lus cDNA

linear EST 05-JUL-2001 clone IMAGE:5050810 5',

EST

Mus musculus Eukaryota; M

Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

house mouse.

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National Institutes of Health, Mammalian Gene
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/strain="FVB/N"
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Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11324 row: o column: 16
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae;
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NIH-MGC http://mgc.nci.nih.gov/.
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/strain="FVB/N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:5132391"
/clone="IMAGE:5132391"
/clone="IDHOB (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pcMv-SPORT6; Site_1: Nt Site_2: Sall; Cloned unidirectionally. Primer: Oliginary in the state of the state
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       cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagc.llnl.gov
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Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/strain="FVB/N"
/db_rref="taxon:10090"
/clone_Tib="NCI_CGAP_Li9"
/clone_tib="NCI_CGAP_Li9"
/clone_tib="NCI_CGAP_Li9"
/lab_host="OHIOB (TI phage-resistant)"
/note="organ: liver; vector: pCMV-SPORT6; Site_1: |
/note="organ: liver; vector: pCMV-SPORT6; Sit
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                                                                                                            TTTGGCCAAGAAAAGTATCCTGGACAAGCTGCACCTCAGCCACGCCCCCATACTCAGTCC 298
                                                                                                                                  Email: Ggapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Plate: LLAM9435 row: g column:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/Clone="ID="NCI_CGAP_L19"
/Clone="ID="NCI_CGAP_L19"
/Lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 253 c 221 g 175 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.0%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 653.8;
Pred. No. 1.8
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ches 12;
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TITLE
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTCAGTACGTGGTGCAGGTGAATGCCAGTGGCTGGTACCAGCTTCTCCCTGGGACCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGC-TCAAGCTGCTTGCA-GCCAGGGACACCTTAC-TCTGGAGCTGGTACCAGAAAGCCA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGTCAGTACGTGGTGCAGGTGAATGCCAGTGGCTGGTACCAGCTTCTCCTGGGACCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGACCTCTCCAGCATCAACCAGACCCGGCTCGAGTTCCACTTCTCTGGTAGAATGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9782 row: 1 column: 08 High quality sequence stop: 659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 975)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602075129F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4212175 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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                                                                   /clone="IMAGE:4212175"
/clone_lib="NCI_CGAP_Li9"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 297 c 266 g 222 t
                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:1000"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                     . 975
41.3%;
97.2%;
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Rodentia;
Score 643.6; DB
Pred. No. 1.4e-1
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                DB 10;
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Matches 698;

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGAGCTGCTTCTCGATTTGGCCAAGAA 276
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
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EST.
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BF236906
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                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                       Unpublished
                                                                                                                                                                        NIH-MGC http://mgc.nc1.nih.gov/.
National Institutes of Health, Mammalian Gene
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                                                                                                                                                                                                                                                                                                                                                                                          ACTCCAACCACAGTGAACCCCCAAAACTGAGGGTCCATGCCCAGCATGTTGGGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGCCCAGGACAGAGTTGAAG-CACTCCCGTTGAGACCCTGAATATAGGGTTTTGGGTCC 107
                                                                                                                                                                                                                                                                            GACCAGAGACAAGAAGAATATGAGATCATCAGCTTTGCTGACACAGACCTCTCCAGCATC
                                                                                                                                                                                                                                                                                                                                               GCTCTCAAGACCGCCTGCAGCGCCCTCCGCGGCCTCGACGGGAAACCCTGTTGGAGCAT 400
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                                                                                                                           GACCAGAGACAAGAAGAATATGAGATCATCAGCTTTGCTGACACAGACCTCTCCAGCATC
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                                                                              AAGAGTTCTTGTGCTAAGACCATATGAC-ACCAACCTCACCTTGACAAGTCAGTACGTGG
                                                                                                                                                             CAGACCCGCTTCATGTTCTTCGTGCAGTTCCCCCACAATGCCACCCAGACCA - TGAATAT
 TGCAGGTGAATGCCAGTGGCTGGTACCAGCTTCTCCT
                                                              AAGAGTTCTTGTGCTAAGACCATATGACTAGCAAACTCACCTTGACAAGTCAGTACGTGG
                                                                                                                                                                                           AACCAGACCCGGCTCGAGTTCCACTTCTCTGGTAGAATGGCCAGTGGCATGGAGGTCCGG
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Plate: LLAM9443 row: c column:
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/clone=lib="NCI_CGAP_Li9"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH108 ('T1 phage-resistant)"
/note="Organ: liver; vector: pCMV-SPORT6; Site_1
Site_2: Sall; Cloned unidirectionally, primer: O
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 189 c 167 g 136 t
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/db_xref="taxon:10090"
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340 CCTGTGTCCAGAGCTGCTTTGAGGACTGCACTGCAGCACCTCCACGGGGTCCCACAGGGG 399
                                         326 CCAGTGTCCAGAGGGGCTCTCAAGACCGCGCTGCAGGGCCTCCGGGGGCCTCGACGGGAA 385
                                                                                                                                                                                                                                                                                                                                                                               100
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                                                                                                                                                                                                                                                                          160 TICTGGCCTTTTCTCCTCCTGGCTCCAACCACAGTGGCCACTCCCAGAGCTGGCGGTCAG 219
                                                                                                                                                                                                                                                                                                                                   147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                         CTGGCCAAGAGAACCATCTTGGACAAGCTGCACCTCACCCGGCGCCAACACTGAACCGC
                                                                                                                                     CTGAGCCCTGAGTCTGTATTGCTCAAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC 159
                                                                                                                                                                                                                                                                                                                                                                                                             CTGAATATAGGCTTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTCCTTGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACACTTCTTCCAGGGCCTCTGGCAGCCAGGACAGAGTTGAGACCACAGCTGTTGAGACC 99
                                                                                                                                                                                TGTCCAGCATGTGGGGGGCCCCACCTTGGAACTGGAGGCCAGCGGGAGCTGCTTCTTGAT 279
                                                                                                                                                                                                                TCCTGG-CTCTTCTGTTCCTGACTCCAACCACAGTAGTGAACCCCAAAAACTGAGGGTCCA 205
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718678
This clone has the following problem: frame shifted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www.shgc.stanford.edu
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Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ייייי ייייביריטיו (משני), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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1 (bases 1 to 1011)
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/clone="IMAGE:4723762"
/tissue_type="tiver"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B"
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243 g 22
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                                                                                                                                                                                                                                                                      Seq primer: -28ml3 rev2 ET from
                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                   quality sequence stop: 480.
/lab_host="DH10B"
                                                                                                      /tissue_type="Liver"
                                                                                                                          /clone_lib="Soares mouse NML"
                                                                                                                                               /clone="IMAGE:680192"
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                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI287120
312 bp mRNA linear EST 24-NOV-1 ui71g11.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1887908 5' similar to SW:IHBC_MOUSE P55104 INHIBIN BETA C CHAIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuq
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI287120.1 GI:3926873
                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
Possible reversed clone: similarity on wrong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 312)
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo.
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91.9%;
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Pred. No. 1.2e-72;
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    JOURNAL
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                          BG566943 541 bp mRNA linear EST 10-APR-2001 602589447F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4723782 5',
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 541)
                                                                                                                                  Homo sapiens
                                                                                                                                                                              EST
                                                                                                                                                                                               BG566943.1 GI:13574596
                                                                                                                                                                                                                       BG566943
                                                                                                                                                                                                                                           mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       performed to exclude fragments (1.5k). Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."

a 94 c 75 g 72 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNI was primed with an oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:1887908"
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Pred. No. 5.1e-62;
0; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 CACATTCCTCCCAGGGTCCCTGGTGCCCAGGACAGAGTTGA-AGCACTCCCGTTGAGAGC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                    GACCTCTCCAGCATCAACCAGACCCGGCTCGAGTTTCCACTT---CTCTGGGTAGAATGGCC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGCCAAGAGAAGCATCTTGGACAAGCTGCACCTCACCCGGCGCCCCAACACTGAACCGC 339
                                                                                                                             GCCTCTCCACCATCAACCAGACTCGTCTTGATTTTCACTTCTCCTCTGATAGAACTGCT 3,6
                                                                                                                                                                                                                                                                        GCACTTCTAGAG---GACAACAGGGAACAGGAATGTGAAATCATCAGCTTTGCTGAGACA 456
GGTGACAGGGAGGTCCAGCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGTGTCCAGAGGGGCTCTCAAGACCGCGCGCGCAGCGCCTCCGCGGGCCTCGACGGGAA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCCAGCATGTGGGGGGGCCCACCTTGGAACTGGAGGCCAGCGGGAGCTGCTTCTTGAT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCCCAGCATGTTGGGGTGCCATCTTTGACCTGGAGAGCCAGCGGGGGGGCTGCTTCTCGGAT\ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGG-CTCTTCTGTTCCTGACTCCAACCACAGTAGTGAACCCCCAAAACTGAGGGTCCA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTGGCCTTTTCTCCTCCTGGCTCCAACCACAGTGGCCACTCCCAGAGCTGGCGGTCAG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAGCCCTGAGTCTGTATGCTC-AAGAAGGGCCTTCCCCAGCAATGACCTCCTCATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAATATAGGCTTTGGGTCCTTTAAGGAGGCTATCCTCCAGCAATGGCCTCCTCCTTGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Organism="Homo sapiens"
/Ob_xref="taxon:9606"
/clone="IMAGE:4723762"
/clone="IMAGE:4723762"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: liver; Vector: pSNR-LIB (Clontech); Site_1:
/note="Organ: liver; Vector: pSNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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75.4%;
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Pred. No. 2.6e-59;
540
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RESULT 14

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                         1063 TGGCAGGGGCTCGTGCCTGCCTACATCTCGGGGGCCCTCTGTCTTTTGCTCTACTATGA 1122
                                                                                                                     1003 TGCCTCCTTTCACACTGCAGTGCTGAATCTGCTCAAAGCCAACGCAGCTGCTGGCACCAC 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                 216 TGCCTCCTTCCATTCTGCCGTCTTTAGCCTCCTCAAAGCCCAACAACCCT-----TGGCC
                                                                                                                                                               823 TCGGGTTCGCCGGCGAGGTATCGATTGCCAGGGGGGGGTCCAGGATGTGCTGTCGACAAGA 882
                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
GTTTTTTGTAGACTTCCGTGAGATTGGCTGGAATGACTGGATCATCCAGCCTGAAGGCTA 942
                                                                                                                                                                                                                                                   CCACTATGTAGACTTCCAGGAGCTGGGGGTGGCGGGATTGGATCCTGCAGCCGGAGGGATA 155
                                                                                                                                                                                                                                                                                                                                   TCGGGCCAGGAGGACGACTCCCACCTGTGAGCCCTGAGACCCCCTTATGTTGTAGGCGAGA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new data is from the 3' end Possible reversed clone: similarity on wrong strand High quality sequence stop: 441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

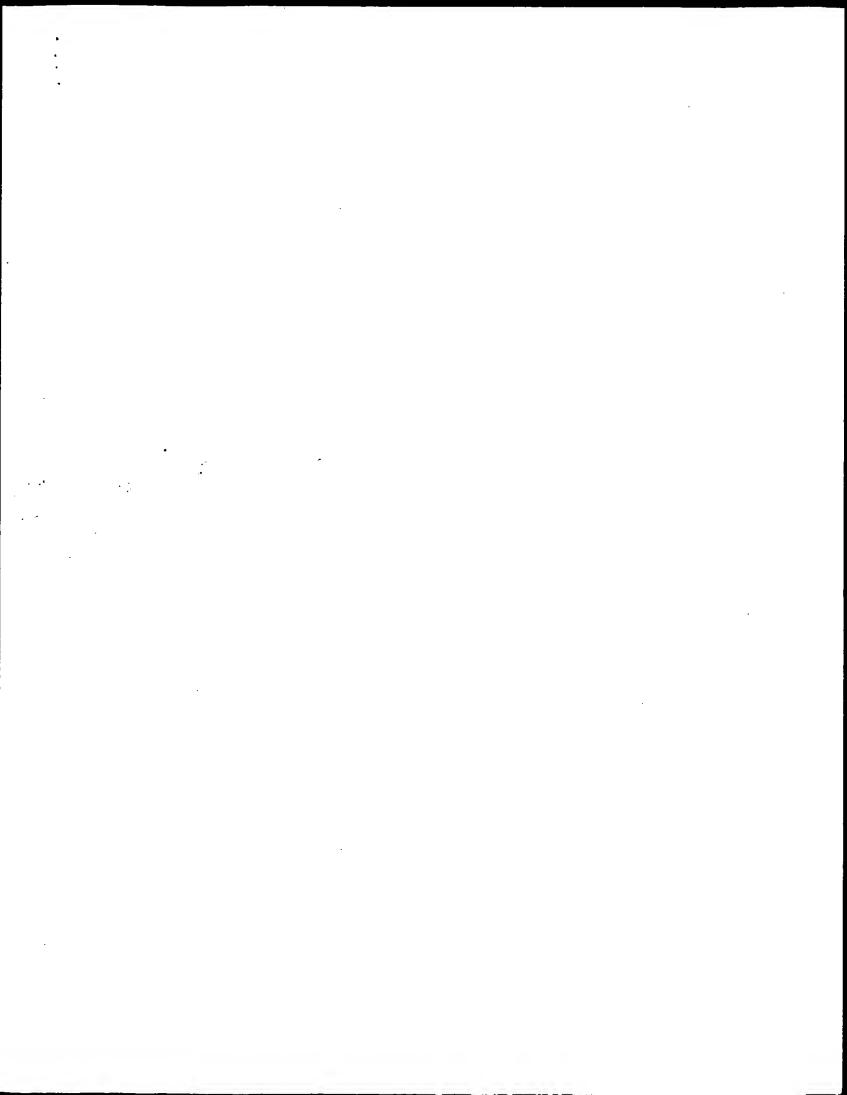
Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
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445 bp mRNA linear EST 09-MAR-19mm08a04.xl Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:520878 3' similar to TR:008717 008717 ACTIVIN BETA E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT. ;, mRNA sequence. AI452079
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1 (bases 1 to 445)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            9.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 145; DB 9;
Pred. No. 1.8e-29;
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KEYWORDS
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AA242421
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AUTHORS
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                                                                                                                                                     Query Match 8.9%;
Best Local Similarity 86.8%;
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                                                                                                                                       Matches 177;
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               1421 CTCCTACATATA---TATGTCATTTTGTCCTAG----CAAACACCCCTTAGCTCCCCTTAG 1474
                                                                                   1361 CTCCTGGGACATGGTTGACCCAGTACACCCATCCTCAGCCTTAAGTTAGAGGCTAATCGA 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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 61
                                                                1 CTCCTGGGACATGGTTGACCCAGTACACCCATCCTCAGCCTTAAGCTAGAGGCTAATCGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mx26a10.rl Soares mouse NML Mus musculus cDNA clone IMAGE:681306 5', mRNA sequence.
AA242421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 314)
Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 243.
    Location/Qualifiers
                                                                                                                                     Conservative
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a 99 c
                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:681306"
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares mouse NML"
/tissue_type="Liver"
                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                  Score 138.4; DB 9; Pred. NO. 1e-27; 0; Mismatches 21;
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                                                                                                                                    21;
                                                                                                                                                                   Length 314;
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Search completed: October 12, 2002, 02:05:01 Job time: 1274.6 secs



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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prinand is derived by analysis of the total score distribution.
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581.5
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                                                                                                                                                                                                                                                            Score
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seq length: 2000000000
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1850
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Gapop 10.0 , Gapext 0.5
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1: /SIDS1/gcgdata/c
2: /SIDS1/gcgdata/c
                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                         747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          1: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
2: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
3: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
4: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
4: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
5: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT: *
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7: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT: *
8: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT: *
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10: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: *
11: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
12: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
13: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
14: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
15: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
16: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
17: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
18: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
19: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
20: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
21: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
22: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
23: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
24: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
25: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
26: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
27: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
28: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
  75.6
75.0
32.1
32.1
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31.6
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29.6
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                            Length
DB
                                        AAW60618
AAP70200
AAY92017
                                                                                                                                                                     AAW60617
AAR89729
AAB70530
                                                                                                                                                                                                                                                            ID
                                                                                                       AAR92754
AAM93672
AAW60619
                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.1.3
Compugen Ltd
                                                                             Murine liver activ
Transforming growt
Human TGF-beta MPI
Human growth diffe
Human polypeptide,
Human liver activi
                   Sequence of porcin
Human inhibin B be
Human activin B su
                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                  being printed,
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N-terminal of inhi	AAP81906	9	116	19.4	359
ш	AAR05444	11	116		363
Sequence of the 14	AAP80020	9	115	19.6	363.5
O	AAR12088	12	116		368
icle stimula	AAR08216		115	19.9	368.5
Second protein cha	AAP71177	æ	115	٠	368.5
	AAP71197		115	19.9	368.5
Human activin A SE	AAY67949		116	20.1	371
	AAR31622		116	20.1	371
Activin AB. Synth	AAR25128		116	20.1	371
Follicle stimulati	AAR08215		116	20.1	371
v	AAR05443	片	116	20.1	371
Polypeptide BUF-3	AAP82061	9	116	20.1	371
Sequence of the 14	AAP80019	ဖ	116	20.1	371
Second protein cha	AAP71176	8	116	20.1	371
Sequence of verteb	AAP71196	8	116	20.1	371
Ю	AAR10990	12	130		372
D	AAR25127	13	116	•	373.5
BUF-4. Synthetic.	AAR31623	14	115	•	373.5
Human KHM-5M. Hom	AAR25129	13	115		373.5
Activin-like pepti	AAR26481		116	•	374
	AAR26482		115	•	374.5
	AAP60520	7	130	21.4	396
EΒΑ	AAB73202		122		398
	AAB73203		121	•	401.5
Sequence of bovine	AAP60518	7	288	•	431
Angiotensin conver	AAU02908	22	303	•	440.5
TGF-beta-like clon	AAR45447	14	87	•	444
=	AAR10991	12	127	•	450
Sequence of porcin	AAP70201	œ	351	•	531
human difi	AAR05413	11	426	29.1	538
activin A	AAY92018	21	426	•	540
qıqu	0	21	426	29.2	540
Sequence of human	AAP70203	œ	426	•	540

ALIGNMENTS

RESULT 1 AAW60617

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Liver activin; beta c; beta e; cell differentiation; haematopoiesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay; menstrual disorder; transgenic; modulator.
                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                     Murine liver activin beta c polypeptide.
                                                                                                                                                                                                                                                                                                                                  AAW60617;
                      Cleavage-site
                                            Domain
                                                                    Modified-site
                                                                                                               Modified-site
                                                                                                                                     Modified-site
                                                                                                                                                           Peptide
                                                                                                                                                                                            Mus sp
                                                                                                                                                                                                                                                                                                                                                        AAW60617 standard;
                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                  /note- "A
                     /note- "F
230..236
                                                                                        /note= "/
/note= "e
237..352
                                            /note=
21..23
                                                                                                              /note= "Asn is putatively N-glycosylated"
143..145
                                                                                                                                     /note= "signal sequence"
111..113
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Protein;
            "endoproteolytic cleavage site'
                                 "propeptide domain"
                                                       "Asn is
                                                                             "Asn is
                                                                                                   "Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                         352
                                                      putatively N-glycosylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents a murine liver activin beta c polypeptide. Sequences CC derived from beta c cDNA clone is used for screening and cloning a liver activin beta e gene. Disorders of cell growth or differentiation (or CC susceptibility to them) are diagnosed by measuring liver activin gene CC activity or by detecting a mutation in the liver activin gene Disorders CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions CC that can be diagnosed using the liver activin. Cell growth and CC compound or agent that upregulates the compound's expression. Antagonists CC can be used to treat liver diseases while agonists can be used to compound may also induce bone growth (e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, or the transgenic animals, are useful for screening for liver activin.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and hacmatopoletic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Fig 1; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-312408/27.
N-PSDB; AAV38237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonadio J, Fang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09822492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNMI ) UNIV MICHIGAN
                                                                                                                                                                  121
301 LLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
                                                                                                  181
                                                                                                                                 181
                                                                                                                                                                                                121
                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                          PILSRPVSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHFS 120
                                                                                            LLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGIDC
                             QGASRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLN
                                                 QGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLN
                                                                                                                                                             GRMASGMEVROTREMEEVQEPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQL
                                                                                                                                                                            GRMASGMEVRQTREMFFVQFPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQL 180
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               352
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Ş.
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                                                                                                                                                                                                                                                                                                                                                                            99.7%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Score 1844; DB 19;
Pred. No. 2.9e-169;
                                                                                                                                                                                                                                                                                                                                                                                           Length 352;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 2
AAR89729
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Best Local :
                                                                                                                         Matches
                                                                                                                                                                                                                                         A cDNA library prepared using total RNA from human liver was subjected to PCR amplification using primers corresp. to conserved regions within the TGF-beta family. Amplification products were subcloned and sequenced: one clone (designated pKK-MP121) was found to contain a new sequence. Part of the insert from the clone was used to re-screen the human liver cDNA library and a 2272 bp fragment coding for a TGF-beta-like protein (i.e. the present sequence) was isolated. This protein has mitrogenic and differentiation-inducing properties making it (or fusion proteins comprising it or heterodimers of the protein with a cystine knot motif protein) useful for inducing tissue regeneration, e.g. for wound healing, inducing growth of health of the protein with a cystine knot motif protein is trustific.
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                               hepatic tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 11; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding transforming growth factor beta MP-121 - has mitogenic and differentiation-inducing activity, e.g. for use in wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IdM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bechtold R, Neidhardt H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JAN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE19511243-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR89729;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor beta MP-121.
 61
                              61
                                                                                                                                      Local Similarity
                                                         PTLNRPVSRAALRTALQHLHGVPQGALLE-DNREQECEIISFAETGLSTINQTRLDFHFS
               PILSRPVSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996-050788/06
                                                                                                                                                                                   352 AA;
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94DE-1423190
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237..352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= mature_protein
                                                                                                                                                                                                                              bone marrow precursor cells, treating fertility
                                                                                                                                    75.6%; Score 1398; DB 17; 76.2%; Pred. No. 2.7e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pohl J, Hoetten
                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ⋛
                                                                                                                                                    DB 17;
                                                                                                                                                    Length 352;
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G-RMASGMEVRQTRFMFFVQFPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQ 179

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RESULT 3
AAB70530
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The present invention describes a protein (I) selected from the members of the transforming growth factor-beta (TGF-beta) superfamily, which is CC monomeric due to substitution or deletion of a cysteine which is CC (II) encoding (I); (2) expression vector (III) containing (II) in a CC guitable vector system; (3) host cell (IV) containing (II) capable of CC producing (I); and (4) a pharmaceutical composition (V) containing (I), CC (II), (III) or (IV). (I) has vulnerary, antiulcer, nootropic, and can be CC used in gene therapy. (V) is useful for the prevention or therapy of CC diseases for which also the dimeric form of the protein would be indicated. Diseases treatable include diseases associated with bone and/or cartilage damage or affecting bone and/or cartilage disease or concluding tendon and/or ligament, periodontal or dental tissue including including tendon and/or ligament, periodontal or dental tissue including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; transforming growth factor-beta; monomeric protein; MP52; MP121; dimeric protein; TGF-beta; vulnerary; antillicer; nootropic; neuroprotective; antilnfertility; osteopathic; gene therapy; bone; cartilage; dental; wound healing; connective tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TGF-beta MP121 protein sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB70530 standard; Protein; 352 AA
                                                                                                                                                                                                                                                                                                                                                              Novel monomeric protein of transforming growth factor-beta family for prevention or therapy of diseases associated with bone, cartilage damage, promotion of wound healing, has substitution or deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF74421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1999;
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                                                                                                                                                                                                                                                                                                            Claim 10; Page 21-22; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYGE-) HYGENE AG C/O MAEDER & BAUMGARTNER TREUH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SDRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "unspecified"
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                                                   Matches 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dental implants, neural tissue including CNS tissue and neuropathological situations, tissue of the sensory system, liver, pancreas, cardiac, blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane, endothelium, epithelium, for promotion or induction of nerve growth, tissue regeneration, angiogenesis, wound healing including ulcers, burns, injuries or skin grafts, induction of proliferation of progenitor cells or bone marrow cells, for maintenance of a state of proliferation or differentiation, for treatment or preservation of tissue or cells for organ or tissue transplantation, for integrity of gastrointestinal lining and for treatment of disturbances in fertility, contraception or pregnancy. The present sequence represents the specifically claimed TGF-beta monomeric protein MP121, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                              Growth differentiation factor-12; GDF-12; liver; cell proliferation; cancer; diagnosis; therapy; transforming growth factor beta.
                                                                                                                                                                                                                                                                                                                                                     Human growth differentiation factor-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR92754 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1996
12-JUL-1995;
                                    01-FEB-1996
                                                                                                                                                               Cleavage; site
                                                                      WO9602559-A1
                                                                                                                                              Region
                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 NLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 CQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 CQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 LPLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 NLLKANTAAGTTGGGSXCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MASSLLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-RMASGMEVRQTREMEFVQFPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILSRPYSRGALKTALORLRGPRRETLLEHDOROEEYEIISFADTDLSSINOTRLEFHFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTSSLLLAFLLLAPTTVATPRAGGOCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTLNRPVSRAALRTALQHLHGVPQGALLE-DNREQECEIISFAETGLSTINQTRLDFHFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
 95WO-US08745
                                                                                                                                              /label= N-glycosylation_site
232..236
237..350
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                          /note= "GFR-12 active C-terminal fragment"
                                                                                                                                 label•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%; Score 1387; DB 22; 75.9%; Pred. No. 3.1e-125; tive 32; Mismatches 51;
                                                                                                                               C-terminal_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 141;
                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping
             EP1130094-A2
                                                                                                            Human polypeptide, SEQ ID NO: 3558
                                                                                                                                          06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human growth differentiation factor-12 (GDF-12 - AAR92754) is a new member of the transforming growth factor beta superfamily that is expressed specifically in liver. It can be obtd. by expression of a CDNA clone (AAT16883) derived from adult liver in transformed host cells. GDF-12 possesses activities that will make it useful in the treatment of liver disorders, e.g. disease states in which liver function is compromised, or cellular proliferative disorders such as hepatocellular carcinoma.
                                           Homo sapiens
                                                                                                                                                                                 AAM93672;
                                                                                                                                                                                                         AAM93672 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding Growth Differentiation Factor-12 - used in diagnostic and therapeutic methods esp. in methods for treating a cell proliferative disorder of liver origin
                                                                                                                                                                                                                                                                                        296 SAVFSLLKANNPWFAST----SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
                                                                                                                                                                                                                                                                                                         296 TAVLNLLKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIDDMVVEACGCS:352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 40-43; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                       236 RTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFH 295
                                                                                                                                                                                                                                                                                                                                                                          236 RGIDCOGGSRMCCRQEFFVDFREIGWNDWIIQPBGYAMNFCTGQCPLHVAGMPGISASFH 295
                                                                                                                                                                                                                                                                                                                                                                                                                       176 SGLRGEKSGVLKLQLDCRPLEGNSTVTGQPRRLLDTAGHQQPFLELKIRANEPGAGRARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 EAQAACSOGHUTLELVPESQVAHSSL-----ILGWFSH-RPFVAAQVRVE--GKHRVRR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Esquela AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 FYQFPHNATQTMNI------RVLVLRPYDTNLTLTSQYVYQVNASGWYQLLLGP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1994;
13-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 HVLPTLPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GSVAPGNGE-----EVISFATVTDSTSAYSSLLTFHLS--TPRSHHLYHARLWL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 ---GPRRETLLEHDQRQEEYEIISFAD-TDLSSINQTRLEFHFSGRMASGMEVRQTRFMF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPPQAALTRALRRLQP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 TEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells in culture and to raise diagnostic antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0311370.
94US-0274215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 594; DB 17;
Pred. No. 8.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GWHTLTLPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
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AAW60619
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
AAW60619 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 Primers useful for synthesizing full length cDNA clones and their
                                                                                           296 SAVFSLLKANNEWPAST----SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS
                                                                                                             296 TAVLNILLKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEAGGCS 352
                                                                                                                                                                        236 RTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYOLNYCSGQCPPHLAGSPGIAASFH
                                                                                                                                                                                                             236 RGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFH
                                                                                                                                                                                                                                                    176 SGLRGEKSGVLKLQLDCRPLEGNSTVTGQPRRLLDTAGHQQPFLELKIRANEPGAGRARR
                                                                                                                                                                                                                                                                                          185 EAQAACSOGHLTLELVPESQVAHSSL-----ILGWFSH-RPFVAAQVRVE--GKHRVRR
                                                                                                                                                                                                                                                                                                                                                                                      137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use in genetic manipulation
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11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
mes 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                          FVQFPHNATQTMNI------RVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGSVCPSCGGSKLAPQAERALVL£LAKQQILDGLHLTSRPRITHPPPQAALTRALRRLQP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR- 80
                                                                                                                                                                                                                                                                                                                                     HVLPTLPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL-----GWHTLTLPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                            GSVAPGNGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GPRRETLLEHDQRQEEYEIISFAD-TDLSSINQTRLEFHFSGRMASGMEVRQTRFMF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa T, Isogai T, Hayashi K, Ishii S,
su A, Sugiyama T, Nagai K, Rojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3558; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                -----EVISFATVTDSTSAYSSLLTFHLS--TPRSHHLYHARLWL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.1%; Score 594; DB 22; 39.3%; Pred. No. 8.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 350;
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T, Koqa
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01-FEB-1999

(first entry)

AAW60619;

Protein; 350 AA

Human liver activin beta e polypeptide.

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This represents a human liver activin beta e polypeptide. The invention CC provides murine beta c and beta e polypeptides and the encoding genes. CC Disorders of cell growth or differentiation (or susceptibility to them) CC are diagnosed by measuring liver activin gene activity or by detecting a CC mutation in the liver activin gene. Disorders of haematopoiesis, CC erythroid differentiation, ovarian follicular maturation, hormone consecretion or cardiac morphogenesis are some conditions that can be CC diagnosed using the liver activin. Cell growth and differentiation can be CC diagnosed using the liver activin. Cell growth and differentiation can be CC upregulates the compound's expression. Antagonists can be used to treat CC upregulates the compound's expression. Antagonists can be used to treat compound compound or agent that CC upregulates while agonists can be used to increase growth and compound compoun
                                                Matches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liver activin; beta c; beta e; cell differentiation; haematopolesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropolesis; haemophilia; cystic fibrosis; immunoassay; menstrual disorder; transgenic; modulator; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9822492-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid encoding sub-units of liver activin useful for regulating growth and differentiation of cells, e.g. for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating liver, bone and haematopoietic disorders
                                                                                                                                                Sequence
22 TEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR- 80
                                                                          Loca L
                                                                          Similarity
                                                                                                                                                350 AA;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0752919
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198..200
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232..236
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237..350
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                                                31.6%; Score 585; DB 19; 38.7%; Pred. No. 6.1e-48; tive 53; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "endoproteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "propeptide domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "mature growth factor domain"
                                                                                                  Length 350;
                                                       Indels
                                                       58; Gaps
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Claim 16; Fig 2; 141pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liver activin; beta c; beta e; cell differentiation; haematopolesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropolesis; haemophilla; cystic fibrosis; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW60618 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         menstrual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine liver activin beta e polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 HYLPTLPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL------GWHTLTLPS 175
                      New isolated nucleic acid encoding sub-units of liver activin -useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders
                                                                                                                                                                                                                                                                 WO9822492-A1
                                                                                  N-PSDB; AAV38238.
                                                                                                WPI; 1998-312408/27
                                                                                                                         Bonadio J,
                                                                                                                                                                               20-NOV-1996;
                                                                                                                                                                                                          20-NOV-1997;
                                                                                                                                                                                                                                      28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 TAVLNILKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 SGLRGEKSGYLKLQLDCRPLEGNSTYTGQPRRLLDTAGHQQPFLELKIRANEPGAGRARR
                                                                                                                                                 (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 TGSVCPSCGGSKLAPQAERALVLELAKQQILEGLHLTSRPRITHPPPQAAVTRALRRLQP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVQFPHNATQTMNI------RVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GPRRETLLEHDQRQEEYEIISFAD-TDLSSINQTRLEFHFSGRMASGMEVRQTRFMF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSVAPGNGE-----EVISFATVTDSTSAYSSLLTFHLS--TPRSHHLYHARLWL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAQAACSQGHLTLELVPESQVAHSSL-----ILGWFSH-RPFVAAQVRVE--GKHRVRR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGGPGIAASFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder; transgenic; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                               96US-0752919
                                                                                                                                                                                                           97WO-US20882
                                                                                                                                                                                                                                                                                                                                                                /note- "F
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237..34
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232..2:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                             . 236
                                                                                                                                                                                                                                                                                                                        "endoproteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                 "Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                              "propeptide domain"
                                                                                                                                                                                                                                                                                            "mature growth factor domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity or by detecting a mutation in the liver activin gene. Disorders CC of haematopolesis, erythroid differentiation, ovarian follicular CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone CC formation, insulin secretion or cardiac morphogenesis are some conditions CC that can be diagnosed using the liver activin. Cell growth and CC compound or agent that upregulates the compound's expression. Antagonists CC can be used to treat liver diseases while agonists can be used to constead in the growth of liver tissue. The liver activin CC compound may also induce bone growth (e.g. for treating baemophilia, cystic fibrosis or menstrual disorders, antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which CC transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, cc modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                          Fertility control; contraception; hormone; spermatogenesis
                                                                                  Sequence of porcine inhibin beta-chain precursor beta-A.
                Sus scrofa domestica
                                                                                                                                  09-APR-1991
                                                                                                                                                                          AAP70200;
                                                                                                                                                                                                          AAP70200 standard; protein; 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                340
                                                                                                                                                                                                                                                                                                                                                      342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This represents a murine liver activin beta e polypeptide. Sequences derived from a beta c cDNA clone is used for screening and cloning the activin beta e gene. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene
                                                                                                                                                                                                                                                                                                                                                                                                                  284 VAGMPGISASFHTAVLNILKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 NASGWYQLLLGPEAQAACSQGHLTLEL....-VPESQVAHSSLILGWF-SHRPFVAAQV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 FQLSPLWSHHL----YHARLWLHVPPSFPGTLYLR--IFRCGTTRCRGFRTFLAEH--QT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 FHFSGRMASGMEVROTRFMFFYQFPHNATQTMNIRVLVLRPYDTNL----TLTSQYVVQV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LLWALVWV------QSRRSACPSCGGPTLAPQGERALVLELAKQQILEGLHLTSRPRIT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVE--GKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLH 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSSGWHPLTLPSSGLRSEDSGVVKLQLEFRPLDLNSTAAGLPRLLLDTAGQQRPFLELKI 223
                                                                                                                                                                                                                                                                                                                                                    PDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RANEPGAGRARRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPH
                                                                                                                                                                                                                                                                                                              PDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                LAGSPGIAASFHSAVFSLLKANNPWPAGS----SCCVPTARRPLSLLYLDHNGNVVKTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPLPQAALTRALRRLQ-PKSMVPGNRE-----KVISFATIIDKSTSTYRSMLT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPVSRGALKTALQRLRGPR-----RETLLEHDQRQEEYEIISFAD--TDLSSINOTRLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.4%; Score 581.5; DB 19; Length 350; 37.7%; Pred. No. 1.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
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                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or
                                       307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
292 ASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC
                                                                                                247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at modulating the climical condt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2B; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulating clinical condition or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1987-137512/20
N-PSDB; AAN70317.
                                                                                                                            203
                                                                                                                                                          187
                                                                                                                                                                                        154
                                                                                                                                                                                                                     127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant human or porcine inhibin or activin - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mason AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1986;
03-OCT-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP222491-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                  10 LLASCWIIVRSSPTPGSGGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                            6 LLALLFLTPTTVVNPKTEG-----PCPACWGAIF--DLESQRELLLDLAKKSILDKLHLS 58
                                                                                                                                                                                                                                                                                                                                                                                                                 ocal
                                                         RVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGIS
                                                                                       CEQCHETGASLVLLGKKKKKEEEAEGRKRDGEGAGVDEEKEQSHRPFLMLQARQSEEHPH
                                                                                                                                                 GSADAGEEAEDVGFPEEKSEVLISEKYVDARKSTWHIFPVSSSIQRLLDQGKSALDIRTA
                              RRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS
                                                                                                                                                                              ------VLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPE 202
                                                                                                                                                                                                                                                                      KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVELEDDIGRRAEM---NELMEQTSEIITF
                                                                                                                          SQVAH----SSLTLG-----
                                                                                                                                                                                                             AEAXGTAXXRKTLRFEISKEGSDLSVVERAEIWLFLKVPKANRTRTKVSIRLFQQQRRPQ
                                                                                                                                                                                                                                          ADTDLSSINQTRLEFHFSGRMASGMEVRQTREMFFVQFPH-NATQT-MNIRVL-----
                                                                                                                                                                                                                                                                                                                                                                                                  133;
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seeburg PH;
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86US-0906729.
85US-0783910.
86US-0827710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="used to design a long synthetic DNA probe" 309..424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="proteolytic processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 550.5; DB 8; Pred. No. 1.7e-44;
                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                            143;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 427;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                          77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY92017 standard; Protein; 407 AA
                                                                                                                                                                                                                                                                                                                                19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 401..407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hairpin loop;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000
Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFS, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
                                                                                                                                                                                                                  WPI; 2000-283585/24.
                                                                                                                                                                                                                                                                       (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352
                                                                                                                                Claim 298; Page 304; 320pp; English.
                                                                                                                                                                        New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g.
                                                                                                                                                                                                                                             Weintraub BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC 426
                                                                        Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bloactivity.
                                                                                                   This is the wild type human inhibin B beta subunit.
                                                                                                                                                           hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                   22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 S 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B beta subunit; CKGF; mutant; cystine knot growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infertility
                                                                                                                                                                                                                                             Szkudlinski MW;
                                                                                                                                                                                                                                                                                                   98WO-US19772.
                                                                                                                                                                                                                                                                                                                                99WO-US05908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329..375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376..400
/label- beta_hairpin_loop_3
/note- "mutant optionally c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label-beta_hairpin_loop_1
/note- "mutant optionally comprises one or more
substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                               "optionally mutated to increase electrostatic interaction between beta hairpin structure an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a receptor*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substitutions in these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interaction a receptor
                                                                                                                                                                                                                                                                                                                                                                                                                   a receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interaction between beta hairpin structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta hairpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure and
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RESULT 10
AAY92019
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THE PROPERTY OF THE PROPERTY O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological activities of the CKGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infertility, time-limited conception and in assisted reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY92019 standard; Protein; 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human activin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human activin B subunit; CKGF; mutant; cystine knot
                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 V--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFIDERLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSEHTAVVNQYRMRGLNPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHASPGADGQERVSEIISFAETDGLASSRVRLYFFISNEGNQNLFVVQASLWLYLKLLPY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRVDGDFLEAVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACLILLAAGWLGPEAWGSPTPPPTPAAPPPPPPPGSPGGSQDTCTSCGG·---FRRPEEL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSLLLALLFL-----TPTTVVNPKTEGP-------CPACWGAIFDLESQREL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVPESQVAHSSLILGWF-----SHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQALFERGERRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------DORQEEYEIISFADTDLSSINQTRLEFHFSGRMASGMEVRQTREMFFVQ-FPH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR-GPRRE---TLLEH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANAA-AGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intertility
                                                                                                                                                                                                                                                                                                                                                               Location/Qualiflers
1..307
                                                                                               329..375
                                                                                                                                                            /label= beta_hairpin_loop_1
/note= "mutant optionally c
                                                             /note=
                                                                                                                                                                                                                                                                                                                                    /note= "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.6%;
33.3%;
                       "optionally mutated to increase electrostatic interaction between beta hairpin structure an
                                                                                                                                                                                                                                                            interaction between a receptor"
                                                                                                                              substitutions in these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 548.5; DB 21;
Pred. No. 2.4e-44;
                                                                                                                                                                   comprises one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145; Indels
                                                                                                                                                                                                                                                                                                     beta
                                                                                                                                     residues"
                                                                                                                                                                                                                                                                                                 hairpin structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
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                                     and
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the wild type human activin B subunit. Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bioactivity.

Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFS, are claimed. The CKGF superfamily comprises at least four families of growth factors; the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members activities of the CKGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 328; Page 305; 320pp; English.
248 LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQ
                                          199
                                                                                                                                                                                                                                                                                                                                                                                                                                                               infertility, time-limited conception and in assisted reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutant cystine knot growth factor proteins comprising one mutant subunits, useful for treating or preventing diseases e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weintraub BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                  128 GHASPGADGQERVSEIISFAETDGLASSRVRLYFFISNEGNQNLFVVQASLWLYLKLLPV 187
                                                                                                                                                                                        91
                                                                                                                                                                                                               68 GRVDGDFLEAVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLD 127
                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                     12 ACLLLLAACWIGPEAWGSPTPPPTPAAPPPPPPPGSPGGSQDTCTSCGG----FRRPEEL 67
                                                                                                                                                                                                                                                                                                                                                                                  Госа1
                                                                                                                                                                                                                                                                                                                       2 ASSLLLALLFL-----TPTTVVNPKTEGP-------CPACWGAIFDLESQREL 42
                                LVPESQVAHSSLILGWF-----SHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQE 251
                                                                     VLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQALFERGERRLN
                                                                                                      ----NATQTMNIRVLVLRPYDTNLTLTSQYVYQVNASGWYQLLLGPEAQAACSQGHLTLE 198
                                                                                                                                                                                                                                              -----LLDLAKKSILDKLHLSORPILSRPVSRGALKTALORLR-GPRRE---TLLEH--
                                                                                                                                                                           -----DQRQEEYEIISFADTDLSSINQTRLEFHFSGRMASGMEVROTRFMFFVQ-FPH 1424
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      407 AA;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Szkudlinski MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US19772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US05908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- beta_hairpin_loop_3
/note- "mutant optionally comprises one or more substitutions in these residues"
401..407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376..400
/label- 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure an
                                                                                                                                                                                                                                                                                                                                                                                29.6%;
                                                                                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                             Score 548.5; DB 2
Pred. No. 2.4e-44;
                                                                                                                                                                                                                                                                                                                                                                Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                             Length 407;
                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             more
                                                                     247
 307
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Matches 124; Best Local Query Match

Similarity

29.48;

Score 543; DB 8; Pred. No. 6.9e-44;

Length 353; Indels

38;

11;

Conservative

64;

Mismatches

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                               A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
 Sequence
                                                                                                                                                                                                                                                                                                                                                                       12-SEP-1986;
03-OCT-1985;
10-FEB-1986;
                                                                                                                                                                                         Disclosure; Fig 9A; 48pp; English.
                                                                                                                                                                                                                               Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology o
                                                                                                                                                                                                                                                                           N-PSDB; AAN70316
                                                                                                                                                                                                                                                                                                                     Mason
                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP222491-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fertility control; contraception; hormone; spermatogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of human inhibin beta-chain precursor beta-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP70204 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP70204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 V--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                        1987-137512/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFVDFREIGWNDWIIQPEGYAMNFCTGOCPLHVAGMPGISASFHTAVLNLLKANAA-AGT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFIDERLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
 353
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A
                                                                                                                                                                                                                                                                                                                                                                     86US-0906729.
85US-0783910.
86US-0827710.
                                                                                                                                                                                                                                                                                                                                                                                                                           86EP-0307586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 38..40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="proteolytic processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="potential N-linked glycosylation sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to design a long synthetic DNA probe"
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AAP70203
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sequence of human inhibin beta-chain precursor beta-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP70203 standard; protein; 426
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fertility control; contraception; hormone; spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 LGPEAQAACSQGHLTLELVPESQVAHSSLILGWF-----SHRPEVAAQVRV-EGKHRVR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 MEVROTREMFEVQ-FPH----NATOTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLL 181
                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 HAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSRVRLYFFISNEGNQN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 CPACWGAIFDLESQREL-----LLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRL 79
                                                                                                                                                                                                                   02-OCT-1986;
                                                                                                                                                                                                                                          20-MAY-1987
                                                                                                                                                                                                                                                                EP222491-A
                                                                                                                                                                     10-FEB-1986;
                                                                                                                                                                                12-SEP-1986;
03-OCT-1985;
                                           Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of
                                                                                N-PSDB; AAN70315
                                                                                               WPI; 1987-137512/20.
                                                                                                                    Mason AJ, Seeburg PH
                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTSCGG----FRRPEELGRVDGDFLEAVKRHILSRLQMRGRPNITHAVPKAAMVTALRKL 56
           Disclosure; Fig 8A; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-GPRRE---TLLEH-----DORQEEYEIISFADTDLSSINGTRLEFHFSGRMASG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTAVLNLLKANAA-AGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGOCPLHVAGMPGISASF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTEAIQALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIR 236
                                                                                                                                                                                                                     86EP-0307586
                                                                                                                                                                      86US-0827710
                                                                                                                                                                                   85US-0783910
                                                                                                                                                                                             86US-0906729
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 165..167
                                                                                                                                                                                                                                                                                                                                                                           /note-"potential N-linked glycosylation sites"
                                                                                                                                                                                                                                                                                        /note="proteolytic processing site"
                                                                                                                                                                                                                                                                                                                             /note-"pro region"
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AAY92016
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Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-necoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                        AAY92016 standard; Protein; 426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 AE---SGTARKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPO 183
                                                                                                                                                                                                                                                                                                       AAY92016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 CEOCOESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 GSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQPLLDQGKSSLDVRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 ADTDLSSINGTRLEFHFSGRMASGMEVROTRFMFFVQFPH-NATQT-MNIRVLVLRPY-- 158
                                                                                  Key Location/Qualifiers Misc-difference 1...325
                                                                                                                                                                            hairpin loop; infertility.
                                                                                                                                                                                             human inhibin A beta subunit; CKGF; mutant; cystine knot growth factor;
                                                                                                                                                                                                                                 Human inhibin A beta subunit.
                                                                                                                                                                                                                                                                      19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 SSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 ISASEHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLLYYDRDSNIVKTDIPDMVVEAC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 PHRRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 KHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 ------DTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLEL--- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEM---NELMEQTSEIITF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                  Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                424 GCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 GCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LLALLELTPTTVVNPKTEG-----PCPACWGAIF--DLESQRELLLDLAKKSILDKLHLS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLASCWITYRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 AA;
                                  /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure are a receptor"
                    326..346
   /label- beta_hairpin_loop_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 540; DB 8; Length 426; 31.2%; Pred. No. 1.7e-43; tive 70; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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Query Match
                                                                                                                                                                                                                                                                      Matches
159 ------: DTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLEL---
: : | |: | | |: : | | : ::
                                                                                                                                                                                                                                                                                                                                               Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                      This is the wild type human inhibin A beta subunit. Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bloactivity.

Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological superfamily comprises at least four familes of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, families are known to be structurally similar (especially comprising the positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological
                                                                                                                                                                                                                                                                                                                                 Sequence
                                               127 AE---SGTARKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQ 183
                                                                                103 ADTDLSSINOTRLEFHFSGRMASGMEVRQTRFMFFVQFPH-NATQT-MNIRVLVLRPY-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 283; Page 303; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weintraub BD, Szkudlinski MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1998;
                                                                                                                                   70
                                                                                                                                                59 ORPILSRPVSRGALKTALORLR....-GPRRETLLEHDQRQEEYEIISF 102
                                                                                                                                                                                 10 LLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 347..394
                                                                                                                                                                                                               6 LLALLFLTPTTVVNPKTEG-----PCPACWGAIF--DLESQRELLLDLAKKSILDKLHLS 58
                                                                                                                                                                                                                                                                                  Local
                                                                                                                  KRPDVTOPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEM---NELMEQTSEIITF 125
                                                                                                                                                                                                                                                                  132;
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                              426 AA;
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US19772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= beta_hairpin_loop_3
/note= "mutant optionally comprises one or more
..._ substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395..419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "mutant optionally comprises one or more
... substitutions in these residues"
                                                                                                                                                                                                                                                                              29.2%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interaction between beta hairpin structure and
                                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                        Score 540; DB 21;
Pred. No. 1.7e-43;
                                                                                                                                                                                                                                                        Mismatches 139;
                                                                                                                                                                                                                                                                                     Length 426;
                                                                                                                                                                                                                                                     Indels
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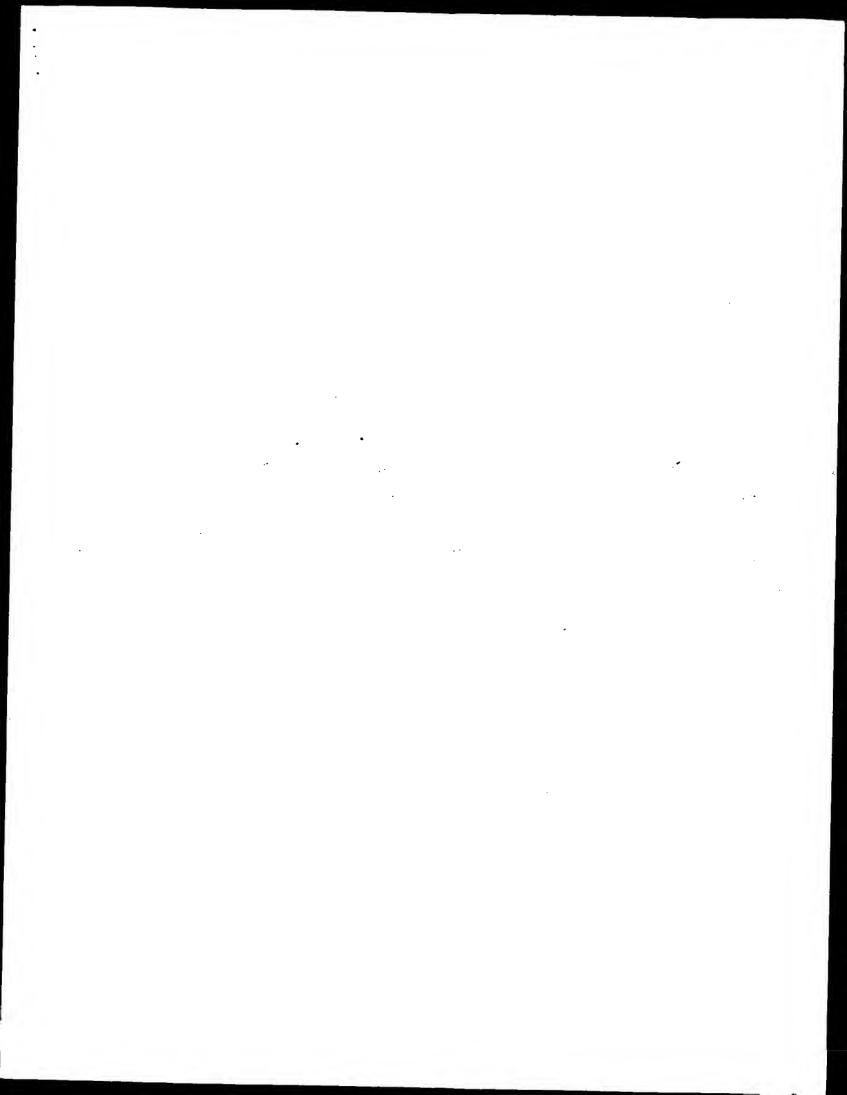
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RESULT 14
AAY92018
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New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g. hypothyroidism and thyroid cancer
                                                               WPI; 2000-283585/24
                                                                                         Weintraub BD, Szkudlinski MW;
                                                                                                                 (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                    22-SEP-1998;
                                                                                                                                                                             19-MAR-1999;
                                                                                                                                                                                                         30-MAR-2000.
                                                                                                                                                                                                                                     WO200017360-A1.
                                                                                                                                                                                                                                                                                                      Misc-difference 420..426
                                                                                                                                                                                                                                                                                                                                                               Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 347..394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hairpin loop; infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human activin A subunit; CKGF; mutant; cystine knot growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human activin A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY92018 standard; Protein; 426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY92018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 GCS 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 SSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 KHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPG 289
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                                                                                                                                                                          80650Sn-OM66
                                                                                                                                                                                                                                                                                                                                        /label = beta_hairpin_loop_3
                                                                                                                                                                                                                                                                                                                              /note= "mutant optionally
                                                                                                                                                                                                                                                                                                                                                              395..419
                                                                                                                                                                                                                                                                                          /note=
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interaction between beta hairpin structure and
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "mutant optionally comprises one or more substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326..346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                             "optionally mutated to increase electrostatic
                                                                                                                                                                                                                                                          interaction between beta hairpin structure a receptor"
                                                                                                                                                                                                                                                                                                             "mutant optionally comprises one or more substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                          a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    _beta_hairpin_loop_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (pDGF) family, the neurotrophins and the transforming growth factor beta family; the families are known to be structurally similar (especially comprising the cystine knot copology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the wild type human activin A subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 313; Page 304; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutants comprise at least one electrostatic charge altering mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta hairpin loop, resulting in increased bloactivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activities of the CKGF.
                                 BUF-3; dhfr; dihydrofolic acid reductase; differentiation
                                                                  BUF-3 human differentiation inducing factor gene product.
                                                                                                                                              AAR05413;
                                                                                                                                                                               AAR05413 standard; protein;
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                                                                                                           27-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADTDLSSINGTRLEEHFSGRMASGMEVRQTREMFEVQEPH-NATGT-MNIRVLVLRPY-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                 PHRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG 363
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                                                                                                           (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physiologically active protein prepn. .
by transforming plasmid having gene coding physiologically active protein and gene of dishydrofolic acid reductase to hamster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene may be expressed by transforming a dhfr negative strain of CHO cells with an active BUF-3 gene and dhfr carrying vector. BUF-3 gene product is a cell differentiating factor.
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                                                            364 SSLSFHSTVINHYRNRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEEC
                                                                                                                         304 PHRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG
                                                                                                                                           230 KHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNECTGQCPLHVAGMPG 289
                                                                                                                                                                                       244 CEQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDH
                                                                                                                                                                                                                      200 VPESQVAHSSLIL-----VEG 229
                                                                                                                                                                                                                                                     184 GSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDVRIA 243
                              350 GCS 352
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                                                                                                                                                                                                                                                                                                                                                   ADTDLSSINGTRLEFHFSGRMASGMEVROTREMFFVQFPH-NATQT-MNIRVLVLRPY-- 158
                                                                                            ISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEAC
   GCS 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.1%; Score 538; DB 11; Length 426; 31.2%; Pred. No. 2.7e-43;
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Search completed: October 12, 2002, 02:06:07 Job time : 43 secs



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OM protein - protein search, using sw model
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Maximum Match 100%
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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PCT-US95-08745-14
US-08-482-577B-24
US-08-289-2222-28
US-09-218-176-7
US-09-054-526B-28
US-09-054-526B-28
US-08-459-850-33
US-08-459-850-43
US-08-459-214-33
US-08-459-214-31
US-08-459-550-41
US-08-459-550-41
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US-09-218-176-4
US-09-218-176-2
US-08-482-577B-2
US-08-289-222E-4
US-09-218-176-2
US-09-054-526B-4
US-08-765-662-14
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122	122	122	122	128	121	121	121	121	121	121	121	121	121	121	147	119	119
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US-08-581-528A-17	US-08-525-596B-27	US-08-455-559-23	US-08-581-529B-17	US-08-455-550-12	PCT-US94-07799-18	PCT-US94-07762-18	PCT-US94-00657-24	US-09-145-060-24	US-09-177-860A-28	US-09-097-616-18	US-08-581-528A-18	US-08-525-596B-28	US-08-455-559-24	US-08-581-529B-18	US-08-065-844A-7	PCT-US95-08745-12	US-09-184-933-12
Sequence 17,	Sequence 27,	•••	Sequence 17,	Sequence 12,	Sequence 18,	Sequence 18,	Sequence 24,	Sequence 24,	Sequence 28,	Sequence 18,	Sequence 18,	Sequence 28,	Sequence 24,	. Œ		12,	Sequence 12,
Appl	Tddv	Iddy	Appl	1ddv	Tddv	Appl	Appl	Tddv	Appl	Appl	Appl	Appl	Appl	Appl	TIddy	Tddv	App1

ALIGNMENTS

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; Sequence 4, ; Patent No. 5
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                                                      US-08-482-577B-4
Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HOTTEN
APPLICANT: NEIDHAI
APPLICANT: BECHTOI
APPLICANT: POHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS NUMBER OF SEQUENCES: 49
                                                                     MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC

ALLUKESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY, STREET: SUITE 330

CITY: WASHINGTON
                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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BECHTOLD, ROLF
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100.0%;
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 Score 1850; DB 1; Pred. No. 1.3e-174;
                  Length 352
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US-09-218-176-4
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APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
                                     APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE TITLE OF INVENTION: TGF- FAMILY NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 92 102 324.8 FILING DATE: 12-FEB-1992
                                                                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: Herewi
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLN
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                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COUNTRY: US ZIP: 20005

Floppy disk

CITY: WASHINGTON

g USA

ADDRESSEE:

STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY, STREET: SUITE 330

NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM

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                                                                                                                                                                                  Sequence 2, Application US/08482577B Patent No. 5807713 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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FILING DATE: 27 MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564
                                                                                       APPLICANT: HOTTEN, GERTRUD APPLICANT: NEIDHARDT, HELGH APPLICANT: BECHTOLD, ROLF APPLICANT: POHL, JENS
                     TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: DE P 44 23 190.3
                                                                                                                                                                                                                                                                                                                                                301 LLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                     301 LLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                NEIDHARDT, HELGE
BECHTOLD, ROLF
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US-08-289-222E-4
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Best Local
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
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                                                                                                                                                                                                                                           APPLICANT: HOTTEN, CONTROL RELIGE APPLICANT: NEIDHARDT, HELGE APPLICANT: BECHTOLD, ROLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                       APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH,
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
                                                                                            CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKALDO, MARMELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
COMPUTER READABLE
                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SDRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 NLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202/638-4810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 CQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 352 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 CQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 LPLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGID 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 LLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGID 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PILSRPVSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFAUTDLSSINQTRLEFHFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MASSILLIALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQR 60
                                                                           CITY: WASHINGTON
                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTSSLLLAFULLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
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                    20005-5701
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linear
                                      USA
FORM:
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                                                                                                                                                                                                                      GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/482,577B
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US-09-218-176-2

Patent No.

6171584

GENERAL INFORMATION:
APPLICANT: H TTEN
APPLICANT: NEIDHA
APPLICANT: BECHTO

H TTEN, Gertrud NEIDHARDT, Helg BECHTOLD, Rolf Sequence 2, Application US/09218176

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Best Local Similarity
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APPLICATION NUMBER: PCT/EP93/
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202,638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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FILING DATE: 07-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
180 LPLGPEAQAACSOGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRRGID 239
                                                                                                                                                                                                                                                          121 G-RMASGMEVROTREMEEVQEPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQ 179
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                                    300 NILKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                              240 CQGGSRMCCRQEFFVDFREIGWHDWIIOPEGYAMNFCIGOCPLHIAGMPGIAASFHTAVL
                                                                                                                    240 CQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVL 299
                                                                                                                                                                                             180 LLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGID 239
                                                                                                                                                                                                                                       120 SDRTAGDREVQQASLMFFVQLPSNTTWTLKVRVLVLGPHNTNLTLATQYLLEVDASGWHQ 179
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                                                                                                                                                                                                                                                                                                                  61 PTLNRPVSRAALRTALQHLHGVPQGALLE-DNREQECETISFAETGLSTINQTRLDFHFS 119
                                                                                                                                                                                                                                                                                                                                                      61 PILSRPYSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                 1 MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MASSLLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: US 08/289,222
12-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.6%; Score 1398; DB 3; 76.2%; Pred. No. 5.6e-130; ative 32; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE P 44 23 190.3
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POHL, Jens

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US-09-218-176-2
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121 G-RMASGMEVROTREMEFVQEPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQ 179
                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
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PRIOR APPLICATION DATA:
08/679,048
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                                61 PTLNRPVSRAALRTALOHLHGVPQGALLE-DNREQECETISFAETGLSTINGTRLDFHFS 119
                                                    61 PILSRPVSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHPS,120
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE TITLE OF INVENTION: TGF- FAMILY
                                                                                                                                                                       / Match 75.6%; Score 1398; DB 4; Local Similarity 76.2%; Pred. No. 5.6e-130; Mismatches 50;
                                                                                                 1 MTSSLLLAFILLAPTTVATPRAGGOCPACGGPTLELESQRELLLDLAKRSILDKLHLTQR 60
                                                                                                                                                                                                                                                                               TOPOLOGY: 11
                                                                                                                                   1 MASSILLALLFLTPTTYVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQR 60
                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 27-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/482,577 FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 2-FEB.
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FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 12-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
STREET: Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                           352 amino acids
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                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                         Length 352;
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Query Match

75.68;

Score 1398;

DB 4;

Length 352

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; TOPOLOGY: 1i; MOLECULE TYPE: US-09-054-526B-4
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                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
                                                                                                                               TELEFAX: 202/638-4810 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 03-APR-199
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY, STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                               TELEPHONE: 202/0-1
TELEPHONE: 202/638-4810
TELEPHONE: TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 NLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 NLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
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                                                      STRANDEDNESS:
                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 CQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 CQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVL 299
                                                                                                                                                                                                                                NAME: KITTS, MONICA CHIN REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                              LENGTH:
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                                                                                       352 amino acids
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BECHTOLD, ROLF
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                                                                                                                                                                        202/638-5000
                   protein
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US-08-765-662-14
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FILING DATE: 12-JULTICATE
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
TELECOMMUNICATION:
TELECOMMUNICATION: 619-678-5079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5929213
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                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 14:
                                                      TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 28-APR-1997
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CORRESPONDENCE ADDRESS:
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                HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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COMPUTER: IF
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                         ENGTH:
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4225 Executive Square, Suite 1400
                                                                                                                                         350 amino acids
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PCT-US95-08745-14
; Sequence 14, Application PC/TUS9508745
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
AMME: Haile, ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/
FILING DATE: 12-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                    HYPOTHETICAL: NO ANTI-SENSE: NO
                                                          MOLECULE TYPE:
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    FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 TAVLNLLKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 RGIDCQGGSRMCCRQEFFYDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 EAQAACSQGHLTLELVPESQVAHSSL-----ILGWFSH-RPFVAAQVRVE--GKHRVRR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 FVQFPHNATQTMNI------RVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLLGP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 SAVFSLLKANNPWPAST----SCCVPTARRPLSLLYLDHNGNVVKTDVPDMYVEACGCS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 RTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFH
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                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                          TELEPHONE: 01, 5099
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COMPUTER: II
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                                                                                   TOPOLOGY:
                                                                                                    STRANDEDNESS: single
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        TELEFAX: 202/538-4810
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: BUITE 330
STREET: WASHINGTON
CITY: WASHINGTON
CTMATE: DC
TTGA
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tent No. 5807713
                                                                                         REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,577B
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOTTEN, GERTRUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 SAVESILKANNPWPAST----SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 TAVLNLLKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 RTPTCEPATPLCCRRDHYVDFQELGWRDWILOPEGYQLNYCSGQCPPHLAGSPGIAASFH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 EAQAACSQGHLTLELVPESQVAHSSL-----ILGWFSH-RPFVAAQVRVE--GKHRVRR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 HVLPTLPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL-------GWHTLTLPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 FVQFPHNATQTMNI-------RVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGP 184
STRANDEDNESS:
                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 ---GPRRETLLEHDQRQEEYEIISFAD-TDLSSINQTRLEFHFSGRMASGMEVRQTRFMF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 TEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 32.1%; Score 594; DB 5; Local Similarity 39.3%; Pred. No. 1.3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGIDCQGGSRMCCRQEFFVDFREIGWNDWIIOPEGYAMNFCTGQCPLHVAGMPGISASFH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCLRGEKSGYLKLQLDCRPLEGNSTYTGQPRKLLDTAGHQQPFLELKIRANEPGAGRARR 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                20005
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655 FIFTEENTH STREET, N.W., G STREET LOBBY
SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIDHARDT, HELGE
BECHTOLD, ROLF
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single
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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-289-222E-28
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APPLICANT: HOTTEN,
APPLICANT: NEIDHARR
APPLICANT: BECHTOLI
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                                                                                                                           TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005-5701

COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, v.

CURRENT APPLICATION DATA;
                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
                                                                                                                                                                                                                           FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DE P 44 23 190.3 FILING DATE: 07-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/289,222 FILING DATE: 12-AUG-1994 PRIOR APPLICATION DATA:
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                                                       STRANDEDNESS
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EPO 92102324.8 FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 25-AUG
                                                                                           LENGTH:
                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY STREET: SUITE 330
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                                                                          amino acid
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                                                                                           106 amino acids
                                                                                                                                                202/638-4810
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BECHTOLD, ROLF
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                 protein
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RESULT 11
US-09-218-176-7
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APPLICATION NUMBER: DE 195 11 243.1 FILLING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MODICA Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE TITLE OF INVENTION: TGF- FAMILY NUMBER OF SEQUENCES: 49
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                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
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FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIfteenth Street, N. W., G Street Lobby.
STREET: Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 30.2%;
Local Similarity 93.4%;
les 99; Conservative
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT, FILING DATE: 2-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
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BECHTOLD, Rolf
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IBM PC compatible
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US-09-054-526B-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                PILING DATE: 12-PEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION UNMBER: 36,105
REFERENCE/DOCKET NUMBER: P564
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                   SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acid
                                                                                                                                                                                                                        FILING DATE: 12-FEB-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: IFILING DATE: 01-JUL-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: DE P 44 23 190.3
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/054,526B FILING DATE: 03-APR-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 CCRQEFFVDEREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY, STREET: SUITE 330 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                     TELEPHONE: 202/038-4810
                                                                                                                                                                                                                                         APPLICATION NUMBER: EPO (FILING DATE: 12-FEB-1992)
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 12-AUG
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                                                                                                                                                                                                          APPLICATION NUMBER:
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5. 6197550
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106 amino acids
nino acid
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BECHTOLD, ROLF
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                                                                                        202/638-5000
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                                                                                                                                                                                                                                                            EPO 92102324.8
                                                                                                                                                                                                          PCT/EP93/00350
                                                         28:
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                                                                                                                          P564-8005
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Patent No. 5525488
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                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958
FILING DATE: 08-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744
              SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acid
                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: 06/827710
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Peter \hat{H}. Seeburg TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and
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APPLICANT:
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                                                                                                                                     NAME: Hasak, Janet E. REGISTRATION NUMBER: 28,616 REFERENCE/DOCKET NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 AAGTTGRGSCCVPTSKRPLSLLYYDRDSNIVKTDIPDMYVEACGCS 352
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                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 460 Point San Bruno Blvd CITY: South San Francisco
STATE: California
                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 06/90 FILING DATE: 31-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/215466 FILING DATE: 05-JUL-1988
                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/197,792
FILING DATE: 16-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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amino acid
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                                                                  910/371-7168
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                                                                                    415/952-9881
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            amino acids
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93.4%;
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US-08-459-850-33
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                                      APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/197792
FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypept
TITLE OF INVENTION: Using such Nucleic Acid
                      PRIOR APPLICATION DATA:
                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          APPLICATION NUMBER: 07/958414 FILING DATE: 08-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 IGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANAA-AGTTGRGSCC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 RKVRVKVYFQEPGHGDRWDVVEKRVDLKRSGWHTLPLTEAIQALFERGERRLNLDVQCDG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 QTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQV 205
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 02-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AHSSLILGWF-----SHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFRE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 LEAVKRHILNRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 LDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR-GPRRE---TLLEH------ 90
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  NUMBER:
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                                                                                                                                                                                                                                                                                                                                   02-JUN-1995
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06/906729
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US-08-459-214-33
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/08459214 Patent No. 5716810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415/225-189
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
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ZIP: 94060
COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 RKVRVKVYFQEPGHGDRWDVVEKRVDLKRSGWHTLPLTEAIQALFERGERRLNLDVQCDG 196
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                                                                                                                        STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callfornia
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                                                                                                COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGQERVSEIISFAETDGLASSRVRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSR 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGWSDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTV--NSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 29.5%; Score 546; DB 1; Length 349; Similarity 35.8%; Pred. No. 7.1e-46;
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amino acid
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Beta Chains of Inhibin and Method for Synthesizing Polypeptide
Using such Nucleic Acid
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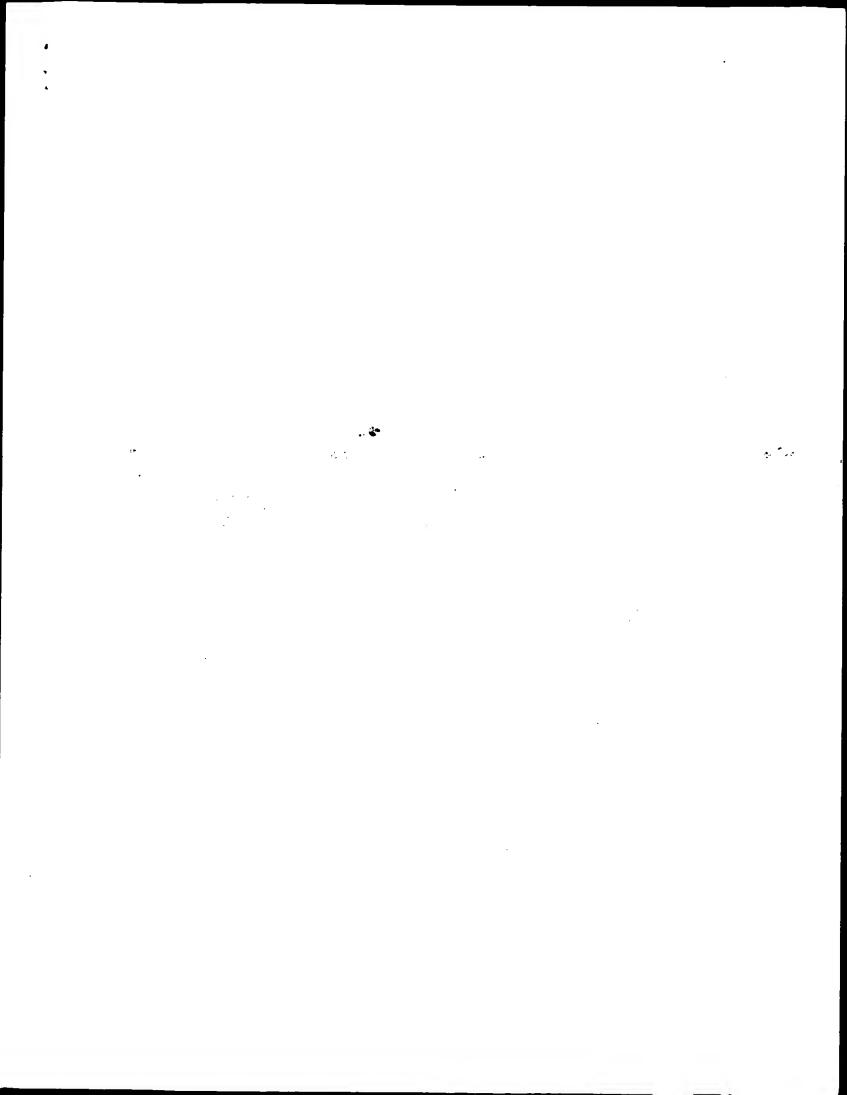
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Best Local 9
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/958414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
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NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: 06/827710
315
                                                                                 257 IGWSDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTV--NSCC
                                                                                                                        259 IGWNDWIIQPEGYAMNECTGOCPLHVAGMPGISASFHTAVLNLLKANAA-AGTTGRGSCC 317
                                                                                                                                                                   197 CQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRL 256
                                                                                                                                                                                             206 AHSSLILGWF-----SHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFRE
                                                                                                                                                                                                                                                       137 RKVRVKVYFQEPGHGDRWDVVEKRVDLKRSGWHTLPLTEAIQALFERGERRLNLDVQCDG 196
                                                                                                                                                                                                                                                                                                146 QTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQV 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                      318 VPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 03-00
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                                                                                                                                                                                                                                                                                                                                           DGQERVSEIISFAETDGLASSRVRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSR 136
IPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA
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03-0CT-1985
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05-JUL-1988
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Search completed: October 12, 2002, 02:10:49 Job time: 16.5 secs



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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>₹</u>
  Pred. No. 1s the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1850
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Gapop 10.0 , Gapext 0.5
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                                           Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
Description
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OY 121 GRMASGMEVRQTREMFFVQFPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQL philififititititititititititititititititit	Oy 1 MASSLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESORELLLDLAKKSILDKLHLSQR	A; Molecule type: DNA A; Residues: 1-352 <fan'> A; Residues: 1-352 <fan'> A; Cross: references: GB: U95962 C; Comment: Activin beta C and beta E form a distinct C; Genetics: A; Introns: 105/3 C; Superfamily: inhibin Query Match Best Local Similarity 100.0%; Score 1850; DB 2 Matches 352; Conservative 0; Mismatches 0</fan'></fan'>	nouse mouse) nce_revision 18-Jul-1997 # ley, E.; Bonadio, J. mmun. 231, 655-661, 1997 mouse activin beta C and b s; MUID:97224404	ALIGNMENTS	30 252.5 13.6 372 2 C39364 31 252.5 13.6 401 2 JH0689 32 249.5 13.5 400 2 A49147 32 249.5 13.5 357 2 A39364 34 248 13.4 454 1 BMU5 35 244.5 13.2 353 2 150607 36 244.5 13.2 353 2 150607 37 244.5 13.2 510 2 A54798 38 243.5 13.2 408 2 \$58791 39 243.5 13.2 513 1 BMU6 40 243 13.1 398 2 JH0688 40 243 13.1 398 2 JH0688 41 243 13.1 398 2 JH0688 42 241.5 13.1 365 2 T43286 43 239 12.9 452 2 149542 44 238.5 12.7 426 2 JH0690
JILTSOYVVQVNASGWYOL 180 ITITSQYVVQVNASGWYOL 180 AAOVRVEGKHRVRRRGIDC 240 ITITSQYKOKHRVRRRGIDC 240 AAOVRVEGKHRVRRRGIDC 240 AAOVRVEGKHRVRRRGIDC 240 ITITITITITITITITITITITITITITITITITITI	LLDLAKKSILDKLHLSQR 60	subset of related activins. ;; Length 352; ;; Indels 0; Gaps 0;	<pre>#text_change 26-Aug-1999 beta E are closely linked and exhl</pre>		GDF-1 embryonic gr bone morphogenetic bone morphogenetic GDF-1 embryonic gr bone morphogenetic osteogenic protein bone morphogenetic vg-1-related prote bone morphogenetic

RESULT 2 \$70580 activin beta C precursor - mouse C;Species: Mus musculus (house mouse)

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C: Keywords: glycoprotein
F:1-18/Domain: signal sequence *status predicted <SIG>
                                                            F;110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                        A:Map position: 2cen-2q13
C:Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                         R;Hoetten, G; Neidhardt, H.; Schneider, C.; Pohl, J. Biochem. Biophys. Res. Commun. 206, 608-613, 1995
A;Title: Cloning of a new member of the TGF-beta family: A putative new activin betaC A;Reference number: JC2466; MUID:95126961
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999
C;Accession: JC2466
                                                                                       F;19-236/Domain: propeptide #status predicted <PRO>F;23-352/Product: activin beta C #status predicted <MAT>
                                                                                                                                                                                                                    A; Cross-references: GDB:632884
                                                                                                                                                                                                                                             A; Gene: GDB: INHBC
                                                                                                                                                                                                                                                                                       A;Residues: 1-352 <HOE>
A;Cross-references: GB:X82540; NID:g669154; PIDN:CAA57890.1; PID:g669155
                                                                                                                                                                                                                                                                                                                                                 A: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: activin beta C chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
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C:Genetics:
A:Introns: 106/1
C/Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-352 <LAU>
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              Best Local Similarity
                                       Query Match
                                                                                                                                                                                                                                                                Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 QGASRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGNPGISASFHTAVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PILSRPVSRGALKTALORLRGPRRETLLEHDORGEEYEIISFADTDLSSINGTRLEFHFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PILSRPVSRGALKTALQRLRGPRRETLLEHDQRQEEYEIISFADTDLSSINQTRLEFHFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGIDC
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              75.6%;
76.2%;
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99.7%;
          Score 1398; DB 2;
Pred. No. 2.3e-120;
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Pred. No. 2.7e-161;
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                        Length 352
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F;254-367/Product: activin beta D chain *status predicted <MAT>
F;64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A:Title: Molecular cloning and functional analysis of a new activin beta subunit: a A:Reference number: JC4151; MUID:95275314
A:Accession: JC4151
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C;Keywords: glycoprotein; mesoderm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: embryo C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: DDBJ:D49543; NID:g961512; PIDN:BAA08494.1; PID:g961513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-367 <ODA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activin beta D chain precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Aug-1995 *sequence_revision 19-Oct-1995 *text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
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284 VAGMPGISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPD 343
                                                      241 AKVHEQSHHATKRSLNCDQNSNLCCRKDYYVDFKDIGWNDWIIKPEGYQINYCMGLCPMH
                                                                                                       225 VRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLH 283
                                                                                                                                                              188 WTGWQTFSLKSMLQTFFDGGNKSLQLELNCDGCQDVPVLANPNN-----SHQPFLVAQ 240
                                                                                                                                                                                                                  174 ASGWYQLLLGPEAQAACSQCHLTLEL-----VPESQVAHSSLILGWFSHRPFVAAQ 224
                                                                                                                                                                                                                                                                         128 TLNFQFTRDKEQSAHVLQAHLWLFFKANRTSQQNETIRLYLVQEAYSRRILISEKL1EPR 187
                                                                                                                                                                                                                                                                                                                             114 RLEFHFSGRMASGMEVRQTRFMFFVQFPHNATQTMNIRVLVLRPYDTNLTLTSQYVVQVN 173
                                                                                                                                                                                                                                                                                                                                                                                    68 PVPRGAVANALRRLHLNKPRMEGLFGSNSWDSNTENTDTDQQSYEIISFAETEYTNENSI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                       66 PVSRGALKTALOR--LRGPRRETLL-----EHDORQEEYEIISFADTDLSSINOT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 LLTLLGALAASTQGLTKKSQCPSCG-----VQDKEVMIELAKQQILQKLHLKERPNITH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 NLLKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMYVEACGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PTLNRPVSRAALRTALOHLHGVPQGALLE-DNREQECELISFAETGLSTINGTRLDFHFS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.8%; Score 699.5; DE 39.3%; Pred. No. 3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65; Mismatches 122; Indels 37;
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C; Species: Mus musculus (house mouse)
C:Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 29-Oct-1999
C; Accession: JC5241; JC5367
R; Fang, J; Yin, W.; Smiley, E.; Wang, S.Q.; Bonadio, J.
Biochem. Biophys. Res. Commun. 228, 669-674, 1996
A; Title: Molecular cloning of the mouse activin beta E subunit gene.
A; Reference number: JC5241; MUID:97096313
A; Contents: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522 R:Fang, J.; Wang, S.; Smiley, E.; Bonadio, J. Blochem. Biophys. Res. Commun. 231, 655-661, 1997 A;Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit A;Reference number: JC5366; MUID:97224404 A;Accession: JC5367
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C: Superfamily:
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A;Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522
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activin beta B subunit - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
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Best Local Similarity
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                                                                                                                                                                                                                                                    342 PDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                         284 LACSPGIAASFHSAVFSLLKANNPWPAGS----SCCVPTARRPLSLLYLDHNGNVVKTDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LLLALLFUTPTTYVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILS 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NASGWYQLLLGPEAQAACSQGHLTLEL-----VPESQVAHSSLILGWF-SHRPFVAAQV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHESGRMASGMEVROTREMEEVQEPHNATQTMNIRVLVLRPYDTNL----TLTSQYVVQV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPLPQAALTRALRRLQ.PKSMVPGNRE.....KVISFATIIDKSTSTYRSMLT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPVSRGALKTALQRLRGPR-----RETLLEHDQRQEEYEIISFAD--TDLSSINQTRLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSSGWHALTLPSSGLRSEDSGVVKLQLEFRPLDLNSTAAGLPRLLLDTAGQQRPFLELKI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQLSPLWSHHL----YHARLWLHVPPSFPGTLYLR--IFRCGTTRCRGFRTFLAEH--QT 163
                                                                                                                                                                                                                                                                                                                                                                                                                     RANEPGAGRARRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPH
                                                                                                                                                                                               PDMVVEACGCS 350
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C;Accession: 151199
R;Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melt Dev. Biol. 157, 474-483, 1993
A;Title: Expression of activin mRNA during early development in Xenopus laevis. A;Reference number: 151199; MUID:93273083
A;Accession: 151199
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A; Residues: 1-370 < DOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: S50899
R;Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
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A; Reference number: $50897; MUID:95112839
A; Accession: $50899
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A; Residues: 1-408 <THO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 SQYVVQVNASGWYQLLLGPEAQAACSQG--HLTLELVPESQVAHSSLIL----GWFSHRP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 KRDVPNMIVDECGCA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 QCPLHVAGMPGISASEHTAVLNLLKANAA-AGTTGRGSCCVPTSRRPLSLLYYDRDSNIV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 FVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 SINQTRLEFHFSGRMASGMEVRQTRFMFFVQFPH---NATQTMNIRVLVLRPYDTNLTLT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 LSRPVSRGALKTALQRLRGPR-RE-----TLLEHD-----QRQEEYEIISFADTDLS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ITHMVPRAAMVSALRKLHAGRVREDGNLEIPDLDGHSLPPPGHSTENSAEIITFAETDDV 117
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                                                                                                   Local Similarity
nes 125; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LLLALLF -- LTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPI 62
52 SQDTCTSCGG----FRRPEELGRVDGDFLEAVKRHILNRLQMRGRPNITHAVPKAAMVTA 107
                                            22 TEGPCPACWGAIFDLESQREL-----LLDLAKKSILDKLHLSQRPILSRPVSRGALKTA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEKKYDIRRSGWHTFPLTEAIQSLFEEGERRLNLEVQCDGCGEYSVIPVYVDPGEESHRP 237
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34.7%; Pred. No. 4.9e-44;
                                                                                                                        29.8%; Score 551; DB 2; Length 408; 34.4%; Pred. No. 1.5e-42;
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                                                                                                        65;
                                                                                                        Mismatches 135;
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A; Residues: 133-411 <ESC>
C; Superfamily: inhibin
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MOI. Endocrinol. 3, 1914-1925, 1989

A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit getal-Reference number: A41398; MUID:90190649

A:Accession: B41398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibin beta-B chain precursor - rat
N;Alternate names: inhibin/activin beta B-chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1992 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: B41398; IS3288; C4905
                                                                                                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Reference number: A40905; MUID:90331931
A:Accession: C40905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin and A;Reference number: I53288; MUID:94307180
A;Accession: I53288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;ESch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, N. Mol. Endocrinol. 1, 388-396, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Dykema, J.C.; Mayo, K.E.
Endocrinology 135, 702-711, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Dykema,
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A; Residues: 1-7 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: I-174 <FEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
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                                                                                                                                                                                                                                                            Matches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 HRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGWPGI 290
  91 ---:---DORQEEYEIISFADTDLSSINQTRLEFHFSGRMASGMEVRQTRFMFFVQ-FPH 142
                                                 72 GRVDGDFLEAVKRHILSRLOLRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLD 131
                                                                                                                                               12 ACLLLLAAGWLGPEAWGSPTPPPSPAAPPPPPPPGAPGGSQDTCTSCGGGGGGFRRPEEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 ASSFHTAVVNQYRMRGLNPGTV--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEEC
                                                                                                   43 ------LLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR-GPRRE---TLLEH-- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 SASFHTAVLNLLKANAA-AGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEAC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 HTFPLTEPIQALFSRGERRLSLDVQCDSCRELAVVPVFVDPGEESHRPFVVVQARLGDSR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 GNQNLFYVQASLWLYLKLLPYYLEKGGRRKVRVKVYGQEQGPGDRWAAVEKRVDLKRSGW 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 MASGMEVROTREMEFVQEPHNATQTMNIRVLVLRPYDTNLTLTSQYV-----VQVNASGW 177
                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                 2 ASSLLLALLFL-----TPTTVVNPKTEGP-------CPACWGAIFDLESQREL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRIRKRGLECDGRTNLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQLLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWF-----SHRPFVAAQVRV-EGK 23,0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LORLR-GPRRE---TLLEH------DQRQEEYEIISFADTDLSSINQTRLEFHFSGR 122
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                              29.7%; Score 549.5; DB 32.8%; Pred. No. 2e-42;
                                                                                                                                                                                                                                                  67; Mismatches
                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                     142;
                                                                                                                                                                                                                                                  Indels 65;
                                                                                                                                                                                                                                                                                                 Length 411;
                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                  12;
                                                                                                                                                                   C; Superfamily: inhibin
                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                           A; Gene: GDB: INHBB
                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S10751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 22-46, 'A', 48-407 <FEN>
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A; Residues: 1-407 < MAS>
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Query Match
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C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone F:1-20/Domain: signal sequence *status predicted <SIG> F:21-292/Domain: propeptide *status predicted <PRO> F:293/Product: inhibin beta-B chain *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 293-294 'GX', 297-302, 'XX', 305-307 <SCH>
C;Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross-references: GB:M31632
A:Experimental source: testis
R:Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, Biochim. Biophys. Acta 1039, 135-141, 1990
A:Title: Purification and characterization of recombinant human activin B.
A:Reference number: S10751; MUID:90304183
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A;Reference number: A90123; MUID:86186863
                                                                                 F;93/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:119347; OMIM:147390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Characterization and regulation of testicular inhibin beta-subunit mRNA. A;Reference number: A40156; MUID:89295443
A;Accession: A40156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 55-407 < MA2>
A; Cross-references: GB_M13437; NID:9186416; PIDN:AAA59169.1; PID:9186417
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000
C;Accession: A40150; C24248; A40156; S10751
C;Accession: A40150; C24248; A50156; S10751
R;Mason, A.J.: Berkemeier, L.M.; Schmelzer, C.H.; Schwall, R.H.
Mol. Endocrinol. 3, 1352-1358, 1989
A:Title: Activin B: precursor sequences, genomic structure and in vitro act.
A:Reference number: A40150; MUID:90114200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibin beta-B chain precursor - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 GRG-----SCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 ----NATOTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYOLLLGPEAQAACSQGHLTLE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 GHASPGADGQERVSEIISFAETDGLASSRVRLYFFVSNEGNQNLFVVQASLWLYLKLLPY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 FFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANAAAGTT 311
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    Score 548.5;
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DB 1;
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C;Comment: Inhibin is secreted by ovaries or contraception; inhibin (C;Superfamily: inhibin (C;Superfamily: inhibin (C;Superfamily: inhibin (Fil-234/Domain: propeptide (Fingment) #status predicted <PROSF:235-349/Product: inhibin beta-B chain #status predicted <PROSF:235-349/Product: inhibin beta-B chain #status predicted <PROSF:235-349/Product: inhibin beta-B chain #status predicted
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Inhibin beta-B chain precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
C;Accession: A01394
R;Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, Nature 318, 659-663, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-349 < MAS>
A; Cross-references: GB: X03267; NID: g2005; PIDN: CAA27021.1; PID: g2006
A; Cross-references: GB: X03267; NID: g2005; PIDN: CAA27021.1; PID: g2006
C; Comment: The source of this protein is ovarian follicular fluid.
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptid lifterent forms of inhibin have been isolated (A and B) that differ in the amino-terminal C; Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follit
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A;Accession: A01394
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                                                                                                                                                                                                                                                                                                  LDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR-GPRRE---TLLEH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQALFERGERRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRVDGDFLEAVKRHILSRLOMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLD 127,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANAA-AGT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHASPGADGQERVSEIISFAETDGLASSRVRLYFFISNEGNQNLFVVQASLWLYLKLLPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSLLLALLFL-----TPTTVVNPKTEGP------CPACWGAIFDLESQREL 42
                                                     RKVRVKVYFQEPGHGDRWDVVEKRVDLKRSGWHTLPLTEAIQALFERGERRLNLDVQCDG 196
                                                                                                      QTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQV 205
                                                                                                                                                            DGQERVSEIISFAETDGLASSRVRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSR 136
                                                                                                                                                                                                               DORQEEYEIISFADTDLSSINGTRLEFHFSGRMASGMEVROTRFMFFVO-FPH----NAT 145
                                                                                                                                                                                                                                                                  LEAVKRHILNRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNOYRMRGLNPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVPESQVAHSSLILGWF-----SHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DQRQEEYEIISFADTDLSSINQTRLEFHFSGRMASGMEVRQTRFMFFVQ-FPH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR-GPRRE---TLLEH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACLLLLAAGWLGPEAWGSPTPPPTPAAPPPPPPPGSPGGSQDTCTSCGG----FRRPEEL 67
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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-SHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFRE
                                                                                                                                                                                                                                                                                                                                                                                                      29.5%; Score 546; DB 1; 35.8%; Pred. No. 3.4e-42;
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                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 349;
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A; Residues: I-424 <MAS>
A; Cross-references: GB:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003
A; Cross-references: GB:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003
C; Comment: The source of this protein is ovarian follicular fluid.
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor polypep ifferent forms of inhibin have been isolated (A and B) that differ in the amino-termi C; Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of fol C; Superfamily: inhibin
C; Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-308/Domain: propeptide #status predicted <PRO>
F; 309-424/Product: inhibin beta-A chain #status predicted <MAT>
F; 165/Binding site: carbohydrate (Asn).(covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibin beta-A chain precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession: A01393
R;Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, Nature 318, 659-663, 1985
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                          424 S 424
                                                                                                                              364 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
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                                                                              S 352
                                                                                                                                                                                 ASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC
                                                                                                                                                                                                                                                                       RVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGIS
                                                                                                                                                                                                                                                                                                                                             CEQCHETGASLVLLGKKKKKEEEAEGRKRDGEGAGVDEEKEQSHRPFLMLQARQSEEHPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADTDLSSINGTRLEFHFSGRMASGMEVRQTRFMFFVQFPH-NATQT-MNIRVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVELEDDIGRRAEM --- NELMEQTSEIITF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLASCWIIVRSSPTPGSGGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLALLFLTPTTVVNPKTEG-----PCPACWGAIF--DLESQRELLLDLAKKSILDKLHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRL 256
                                                                                                                                                                                                                                       RRRRRGLECDGKVNICCKKOFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS
                                                                                                                                                                                                                                                                                                                                                                                                SQVAH----SSLILG-----VESHRPFVAAQVR--VEGKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSADAGEEAEDVGFPEEKSEVLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSALDIRTA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEAGTA---RKTLRFEISKEGSDLSVVERAEIWLFLKVPKANRTRTKVSIRLFQQQRRPQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 8.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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423 351 291 303

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A;Status: processing A;Molecule type: mRNA
A;Residues: 311-376,'AC',380-426 <BER>
A;Cross-references: EMBL:X72498; NID:g297786; PIDN:CAA51163.1; PID:g755740
A;Cross-references: EMBL:X72498; NID:g297786; PIDN:CAA51163.1; PID:g755740
A;Cross-reference, EMBL:X72498; NID:g297786; PIDN:CAA51163.1; PID:g755740
A;Cross-reference number: PN0010; MJID:g1144591
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A; Residues: 311-426 <STE>
A; Cross-references: GB:X04447; NID:g33928; PIDN:CAA28041.1;
A; Mason, A.J.; Niall, H.D.; Seeburg, P.H.
Blochem. Blophys. Res. Commun. 135, 957-964, 1986
A; Title: Structure of two human ovarian inhibins.
A; Reference number: A90123; MUID:86186863
A; Accession: B24248
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A;Title: Erythroid differentiation factor is encoded by the sakeference number: A30884; MUID:88190086
A;Accession: A30884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X57578; NID:g28351; PIDN:CAA40805.1; PID:g825621 A;Note: the authors translated the codon GAG for residue 53 as Gly and GAV R;Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G FEBS Lett. 206, 329-334, 1986
A;Title: Human inhibin genes. Genomic characterisation and sequencing. A;Reference number: A91366; MUID:87005283
A;Accession: B23556
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross·references: GDB:1:
A;Map position: 7p15-7p13
A;Introns: 129/3
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 311-313 'X', 315-320, 'XX', 323-328, 'X', 330-334 <FUJ>
C; Comment: Activins A and B are homodimers of inhibin beta-A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:J03634; NID:g181946; PIDN:AAA35787.1; R;Bergy H.; Walter, M.; Northemann, W. submitted to the EMBL Data Library, April 1993 A;Description: Nucleotide sequence coding for the mature subu A;Reference number: S33351 A;Accession: S33351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Seq. 2, 103-110, 1991
A;Title: Structure and sequence analysis of the human activin beta(A) subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: INHBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bin beta-A and beta-B, respectively.
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A; Residues: 1-426 < MUR>
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A; Residues: 1-426 <MAS>
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A; Residues: 1-426 <TAN>
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A;Accession: S30488
                                                                                  ;Introns: 1477
;Superfamily: Inhibin
;Superfamily: Inhibin
;Keywords: 91/coprotein; gonad; heterodimer; homodimer;
;1-28/Domain: signal sequence #status predicted <SIG>
;1-28/Domain: signal sequence #status predicted <PRO>
;29-310/Domain: propeptide #status predicted <PRO>
;311-426/Product: inhibin beta A chain #status experimental <MAT>
;311-426/Product: inhibin beta A chain #status predicter
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                                                Length 426;
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R:Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack, Development 110, 435-443, 1990
A;Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia A;Reference number: A60087; MUID:92155098
A;Accession: A60087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibin beta-A chain - mouse
N;Alternate names: activin A; mesoderm-inducing factor WEHI-MIF
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: A60087; I48265; S31440
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C; Superfamily: inhit
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Development 117, 711-723, 1993
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A; Residues: 309-311,'X',313-318,'XX',321-325
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HLKKRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEM - - - NELMEQTSEI
                     LLASCWIIVRSSPTPGSEGHGSAPDCPSC--ALATLPKDGPNSQPE-MVEAVKKHILNML
                                                                                                    LLALLELTPTTVVNPKTEG-----PCPACWGAIFDL----ESQRELLLDLAKKSILDKL
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                                                                                                                                       Similarity 32.
36; Conservative
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32.1%;
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                                                                                                                                         68;
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Pred, No. 2.4e-41
B; Mismatches 13
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0; Mismatches
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ches 139;
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                      GPRRETLLEHDQRQEEYEI 99
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A; Residues: 1-393 <WIT>
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                                                                                                                    249 LVDPSDPSHRPFLVVRAQQADGKHRIRKRGLECDGNNGGLCCRQQFYIDFRLIGWNDWII 308
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                                        309 APAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQYRMRGMSPGSV--NSCCIPTKLSTM 366
                                                                                                                                                                                                                                         163 TLTSQYV------VQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQVAHSSLILGW 214
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                                                                                                                                                                                                    ---GQNVHWPMMEKRVELKRSGWHTFPVSEAIREMLAKGGRRQDLDIHCEGCEAANVLPI 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPHRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIACEQCQESGASLVLLGKKKKKEVDGDGKKKDGSDGGLEEEKEQSHRPFLMLQARQSED 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDLSSINQTRLEFHFSGRMASGMEVRQTR-FMFFVQFPHNATQTMNIRVLV-LRPYDTNL 162
                                                                                                                                                                                                                                                                                                                                                               MRERPNITHPIPKAAMVTALRKLHAGKVREDGRVEIPNLDGHAAHNEVQEETSEIISFAE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                             LSVTCLMACLLSVQCSSLGAETGSQESQCVSCGLGHQEDSGRMDTDFLEAVKRHILNRLQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPQGSLDTGDEAEEMGLKGERSELLLSEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISFADTDLSSINGTRLEFHESGRMASGMEVRQTRFMFFVQFPH-NATQT-MNIRVLVLRP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y-----CTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLEL 199
                                                                            QPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANA-AAGTTGRGSCCVPTSRRPL
                                                                                                                                                            F-----SHRPFVAAQV-RVEGKHRVRRRGIDCQGGS-RMCCRQEFFVDFREIGWNDWII 266
                                                                                                                                                                                                                                                                                   SDDVTPSKSSLYFLISNEGNQNLYVLQANLWLYFKLMPGTLEKGLRAKVTVRVHSYEPG- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 533.5; DB 2;
Pred. No. 5.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 139;
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A; Residues: 1-425 <THO>
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A; Molecule type: mRNA
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C:Superfamily: inhibin
C:Keywords: disulfide bond: glycoprotein; gonad; heterodimer; homodimer; hormone
C:Keywords: disulfide bond: glycoprotein; gonad; heterodimer; homodimer; hormone
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-309/Domain: propeptide #status predicted <PRO>
F:310-425/Product: beta-A inhibin/activin #status experimental <MAT>
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Reference number: S50897; MUID:95112839
A;Accession: S50898
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A:Residues: 310-312,'X',314-319,'XX',322-328,'P' <CHE>
R;Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, Mol. Cell. Endocrinol. 44, 55-60, 1986
A:Title: Isolation of boyine follicular fluid inhibin of about 32 kDa.
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A;Title: Cloning and sequence analysis of cDNA species coding for the two subunits of A;Reference number: A94097; MUID:86205842
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GSLDAGEEAEEVGLKGEKSEMLISEKVVDARKSTWHIFPVSSCIQRLLDQGKSSLDIRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                           -----DTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLEL--- 199
                                                                                                                                                                                                                                                                                           AE---SGTARKTLHFEISKEGSDLSVVERAEIWLFLKVPKANRTRSKVTIRLFQQQKHLQ
                                                                                                                                                                                                                                                                                                                                                                                                         ADTDLSSINGTRLEFHFSGRMASGMEVRQTREMEFVQFPH-NATQT-MNIRVLVLRPY-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEM---NELMEQTSEIITF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRPILSRPVSRGALKTALQRLR--------GPRRETLLEHDQRQEEYEIISF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.8%; Score 532.5; DB 1; 31.0%; Pred. No. 7.7e-41; tive 70; Mismatches 140;
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	Scarch completed: October 12, 2002, 02:09:56 Job time : 28 secs	earch co	J. S
	424 CS 425		g
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423	364 SLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECG 423		В
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363	304 HRRRRGLECDGKVNICCKKOFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGS 363		Db
290	231 HRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGI 290		γo
303	244 CEOCOETGASLVLLGKKKKKEEEEGEGKKRDGEGGAGGDEEKEOSHRPFLMLQAROSEDHP 303		ДĎ
230	200 VPESQVAHSSLIL		Ş

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Minimum DB seq length: 0
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    Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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SMART; SM00204; TGFB; 1.
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SMART; SM00204; TGFB; 1.
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submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: INHIBINS AND ACTIVINS INHIBITY AND ACTIVATE,
-:- FUNCTION: THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
SUBGURIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                           SEQUENCE
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                                                                11;
                                                                                                                                    INHIBIN BETA C CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                             Score 1621.5; DB 1
Pred. No. 2.4e-143;
1; Mismatches 25;
                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                        6B219BF6C3E180A1 CRC64;
                                                                                           DB 1;
                                                             Indels
                                                                                        Length 351;
                                                             1;
                                                           Gaps
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01-OCT-1996
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas T.Z., Chapman S.M., Hong W., Gurusingfhe C., Mellor S.L., Fletcher R., Pedersen J., Risbridger G.P.; "Inhibins, activins, and follistatins: expression of mRNAs and cellular localization in tissues from men with benign prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCDLINE-95126961; PubMed-7826378;
HOCTTEN G., Neidhardt H., Schneider C., Pohl J.;
"Cloning of a new member of the TGF-beta family: a
activin beta C chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Inhibin beta C chain precursor (Activin beta-C chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMUH
                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY.
MEDLINE-98089987; PubMed-9428386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blochem. Blophys. Res. Commun. 206:608-613(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                               use by non-profit institutions as long as its content is in no, way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate 34:34-43(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperplasia.";
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                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                         TISSUE SPECIFICITY: EXPRESSED IN BENIGN PROSTATIC HYPERPLASIA SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBINS ARE HETERODIMERS OF ORE ALPHA AND ONE BETA SUBUNIT. ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRRGIDC
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                                                                                                                                                                                                                                                                                                                                                      SUBUNIT
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 X82540;
                                                                                                                                                                                                                                                                                                                                                    COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS
 CAA57890.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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DISULFID
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16-OCT-2001
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00438; GFCYSKNOT. PRINTS; PR00672; INHIBINBC.
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                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002400; GF_cysknot.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
               Submitted
                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                         TISSUE-Rhabdomyosarcoma;
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                   Inhibin beta
                                                                                       NCBI_TaxID=9606;
                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                              THBE_HUMAN
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FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                      NLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 76.2
69: Conservative
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               (MAR-2001) to
                                                                                                                                                                 (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat)
E chain precursor (Activin het
INHIBINS
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161
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76.2%;
                                                                                                        Primates;
                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38238 MW;
                                                                                                                                                                 precursor (Activin beta-E chain).
AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
               the
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a EMBL/GenBank/DDBJ databases
ACTIVINS INHIBIT AND ACTIVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
1-LINKED (GLCNAC. ..) (POTENTIAL)
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BY SIMILARITY.
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                                                                                                        Craniata; V
Catarrhini;
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                                                                                                                        Vertebrata; Euteleostomi;
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Best Local :
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SEQUENCE
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CHAIN
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SIGNAL
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PRINTS: PRO0672; INHIBINBC.
PRODOM: PD0000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001839; TGF-beta. Pfam; PF00019; TGF-beta; 1.
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InterPro; IPR001318; Inhibin_betaC.
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SAVESLLKANNPWPAST...-SCCVPTARRPLSLLYLDHNGNYVKTDVPDMVVEACGCS 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPPQAALTRALRRLQP 81
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meen the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
fied and this statement is not removed. Usage by and for com-
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                                                            TAVLNLLKANA -- AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                            RTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFH
                                                                                                                                                           RGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFH @95,
                                                                                                                                                                                                                                                SGLRGEKSGVLKLQLDCRPLEGNSTVTGQPRRLLDTAGHQQPFLELKIRANEPGAGRARR
                                                                                                                                                                                                                                                                                                          EAQAACSQGHLTLELVPESQVAHSSL-----ILGWFSH-RPFVAAQVRVE--GKHRVRR
                                                                                                                                                                                                                                                                                                                                                                      HVLPTLPGTLCLRIFRWGPRRRRQGSRTLLAEHHITNL------GWHTLTLPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                             FVQFPHNATQTMNI------RVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSVAPGNGE-----EVISFATVTDSTSAYSSLLTFHLS--TPRSHHLYHARLWL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GPRRETLLEHDQRQEEYEIISFAD-TDLSSINQTRLEFHFSGRMASGMEVRQTRFMF:136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR- 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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350
248
315
347
349
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 9.3e-48;
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: A49C1495677E3E6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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MBL outstation -
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                 DISULFID
DISULFID
DISULFID
DISULFID
                                                                                   CHAIN
                                                                                                                       SIGNAL
                                                                                                                                                   ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROSSMANITH W., Peter B., Schulte-Hermann R.;

"Rat activin beta C and beta E: sequence and expression.";

"Rat activin beta C and beta E: sequence and expression.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVARY GLAND.

RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND TUTUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,

EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
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O88959; Q9R285;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat Inhibin beta E chain precursor (Activin bet
   DISULFID
                                                                                                                                        Growth
                                                                                                                                                                                                      Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00672; INHIBINBC.
                                                                                                                                                                                                                                                                                                           EMBL; AF089825; AAC36741.1;
EMBL; AF140032; AAD30133.1;
HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Kretser D.M.;
de Kretser D.M.;
"Cloning and regulation of the rat activin betaE subunit.";
"J. Mol. Endocrinol. 24:409-418(2000).
                                                                                                    PROPEP
                                                                                                                                                                                                                                                         InterPro; IPR002400; GF_cysknot.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver, and MEDLINE=20290891; PubMed=10828834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Bryan M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVINS.

SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT. ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                       factor;
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                                                                                                                                     Hormone;
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Rodentia;
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                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerdprasert O.,
             POTENTIAL.
INHIBIN BETA E |
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
                                                                                                                     POTENTIAL.
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                                                                                                                                   Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hedger M.P.,
                                                                                   CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTIONS
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                 Fang J., Wang S.Q., Smiley E., Bonadio J.;
Fang J., Wang J., Wang J.;
Fang J., Wang J.;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalla; Eutheria; R
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                                                                                                                                                                                                                                                                                                                   MEDLINE-97224404; PubMed-9070865;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Fang J., Yin W., Smiley E., Wang S.O., Bonadio J.;
*Molecular cloning of the mouse activin beta E subunit gene.";
Biochem. Biophys. Res. Commun. 228:669-674(1996).
                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fang J., Yin W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97096313; PubMed-8941337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta E chain precursor (Activin beta-E chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLWALAWV-----QSTRSACPSCGAPTLTPQGERALVLELAKQQILEGLHLTSRPRIT 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGIAASFHSAVFSLLKANNPWPAGS----SCCVPTARRPLSLLYLDHNGNVVKTDVPDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGISASFHTAVLNLLKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGM 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTLPSSGLRSEESGVTKLQLEFRPLDLNSTTARLPRLLLDTAG--QQRPFLELKIRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLLLGPEAQAACSQG--HLTLELVP---ESQVAHSSLIL----GWFSHRPFVAAQVRVE- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQLSPLWSHHLYHARLWLHV--PPSFPATLYLRIFGCGTTRCRGSRTFLAEHQTTSSGWH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSGRMASGMEVROTREMEEVQEPHNATQTMNIRVLVLRPYDINLILISQYVVQVNASGWY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPLPQAALTRALRRLQ.PRSMVPGNRE...-.KVISFATSIDKSTSTYRSVLT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGAGRARRTPTCESETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGS
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44; Conservative
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350 AA;
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161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38898
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39.2%;
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EH -> DY (IN REF. 2)
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Best Local
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PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00672; INHIBINBC.
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002400; GF_cysknot.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:109269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U96386; AAB53801.1;
                                               342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: FIRST EXPRESSION IN EMBRYONIC LIVER IS DETECTED AT DAY E17.5.
                                                                                                                                                                                                                                                                                                                                                                  NASGWYQLLLGPEAQAACSQGHLTLEL------VPESQVAHSSLILGWF-SHRPFVAAQV
                                                                                                                            RVE--GKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLH
                                                                                                                                                                                                                                                                                                                   TSSGWHALTLPSSGLRSEDSGVVKLQLEFRPLDLNSTAAGLPRLLLDTAGQQRPFLELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPVSRGALKTALQRLRGPR-----RETLLEHDQRQEEYEIISFAD--TDLSSINQTRLE 116
PDMVVEACGCS
                                               PDMVVEACGCS 352
                                                                                                    LAGSPGIAASFHSAVFSLLKANNPWPAGS---
                                                                                                                                                                                                           RANEPGAGRARRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPH
                                                                                                                                                                                                                                                                                                                                                                                                                       FQLSPLWSHHL - - - - YHARLWLHVPPSFPGTLYLR - - IFRCGTTRCRGFRTFLAEH - - QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHFSGRMASGMEVROTREMFFVQFPHNATQTMNIRVLVLRPYDTNL----TLTSQYVVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPLPQAALTRALRRLQ-PKSMVPGNRE------KVISFATIIDKSTSTYRSMLT 111
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 1.4e-46;
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N-LINKED (GLCNAC. . .) (PO:
; F37C76C8061D8AD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INHIBIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                       -SCCVPTARRPLSLLYLDHNGNVVKTDV
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                                                                                                                                                                                                                                                                                                                                                                                                                       163
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IHBB_CHICK
                                                                                                       InterPro; IPR002440; GF_cysknot.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
SMAN...
PROSITE; FU.
PROSITE; HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHBB_CHICK STAN
P27093; O73796;
O1-AUG-1992 (Rel. 2
O1-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT COMPOSITION. INHIBING FILE.

ACTIVINS.

-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BON INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.

ACTIVIN B IS A HOMODIMER OF BETA-B.

ACTIVIN B IS A DIMER OF BETA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 311-381 FROM N.A.

MEDILINE-91029482; PubMed-225063;

Mitran1 E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., B

"Activin can induce the formation of axial structures and
in the hypoblast of the chick.";

Cell 63:495-501(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WHITE
Hecht D.J., D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klinger H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

GONADAL HORMONE SECRETION, INSULIN SECRETION, NERVE CELL SURVIVAL,

ERYTHROID DIFFERENTIATION, INSULIN SECRETION, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                    M61166; AAA48568.1; -. M57408; AAA03079.1; -. P18075; 18MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF055478; AAC14187.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z71594; CAA96248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
             PS00250; TGF_BETA_1; 1.
actor; Hormone; Glycoprotein; Signal.
1 25 POTENTIAL.
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J., Davis A.J.,
d (MAR-1998) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    el. 40, Last annotation update)
chain precursor (Activin beta-B chain).
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35, Last sequence up
40, Last annotation
(Activ)
                                                                                                                                                                                                                                                                             GF_cysknot.; TGF-beta.; TGFb_N.
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.. Ryan I.M., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ryan
the F
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Best Local
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                                                                                                                                                                                                                                                           P42917;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta B chain precursor (Activin beta-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
CARBOHYD
CONFLICT
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CHAIN
DISULFID
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                                                                                     Thompson D.A., Cronin C.N., Martin F.;
Thompson D.A., Cronin C.N., Martin F.;
"Genomic cloning and sequence analyses of the bovine alpha-, beta and beta B-inhibin/activin genes. Identification of transcription factor AP-2-binding sites in the 5'-flanking regions by DNase I
                                                                                                                                                                                                                          Bos taurus (Bovine)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                               TISSUE-Liver;
                                                                            footprinting.";
                                                                                                                                               MEDLINE-95112839; PubMed-7813465;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                  NCBI_TaxID-9913;
                                                                                                                                                                                                                Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MASSLLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELL----LDLAKKSILDKLH 56
          FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLANG INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
                                                                                                                                                                                                                                                                                                                                                                                                                 MLYFDDEYNIVKRDVPNMIVEECGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                         LLYYDRDSNIVKTDIPDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTV--NSCCIPTKLSTMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANAA-AGTTGRGSCCVPTSRRPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GWFSHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSQRPILSRPVSRGALKTALQRLRGPRRETLLEHDQRQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LACGLLLLGAAATPTP--PPAGSSPQDTCTSCGFRRPEEPGKVDGDFLEAVKRHILSRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISFAETDDLASSRVRLYFFISNEGNONLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISFADTDLSSINQTRLEFHFSGRMASGMEVRQTRFMFFVQ-FPH----NATQTMNIRVLV
                                                                Biochem. 226:751-764(1994).
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P -> PG (IN REF.
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                                                                                                                                                                                                                            Bovoidea;
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                                      GLAND
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID DISULFID
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00671; INHIBINBB.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U16240; AAB6
HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U16241; AAB60628.1; -. EMBL; U16240; AAB60628.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPRO01839; TGF-beta.
InterPro; IPRO01111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002400; GF_cysknot.
348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-B AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVINS.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                           LQRLR-GPRRE---TLLEH------DQRQEEYEIISFADTDLSSINQTRLEFHFSGR 122
                            SASFHTAVLNLLKANAA-AGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEAC
                                                                                  HRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGI 290
                                                                                                                                                                                                                                                            GNONLFVVQASLWLYLKLLPYVLEKGGRRKVRVKVYGQEQGPGDRWAAVEKRVDLKRSGW
                                                                                                                                                                                                                                                                                                   MASGMEVROTREMEEVOEPHNATOTMNIRVLVLRPYDTNLTLTSQYV-----VQVNASGW 177
                                                                                                                                                                                                                                                                                                                                               LRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSRVRLYFFISNE
                                                                                                                                                                                                                                                                                                                                                                                                                                    SQDTCTSCGG----FRRPEELGRVDGDFLEAVKRHILNRLQMRGRPNITHAVPKAAMVTA 107
ASSFHTAVVNQYRMRGLNPGTV--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEEC
                                                                                                                                                                       HTFPLTEPIQALFSRGERRLSLDVQCDSCRELAVVPVFVDPGEESHRPFVVVQARLGDSR
                                                                                                                                                                                                                 YQLLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWF-----SHRPFVAAQVRV-EGK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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408
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Pred. No. 1.1e-43;
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N-LINKED (GLCNAC. . .) (PC
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                         349
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> MIM; 147390; HSSP; P18075; 1BMP.

InterPro; IPR002400; GF_cysknot.
InterPro; IPR000381; Inhibin_betaB

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RESULT 9
1HBB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mason A.J., Niall H.D., Seeburg P.H.;

"Structure of two human ovarian inhibins.";

Blochem. Blophys. Res. Commun. 135:957-964(1986).

-I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

-RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Inhibin beta B chain precursor (Activin beta-B chain).
EMBL; M31669; AAA59451.1; -. EMBL; M31668; AAA59451.1; JOINED. EMBL; M31682; AAA59170.1; -. EMBL; M13437; AAA59169.1; -. PIR; C24248; C24248.
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 55-407 FROM N.A. MEDLINE-86186863; PubMed-3754442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization and regulation of testicular inhibin beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 22-407 FROM N.A. MEDLINE-89295443; Pubmed-2739657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activities."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mason A.J., Berkemeier L.M., Schwelzer C.H., "Activin B: precursor sequences, genomic stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-90114200; PubMed-2575216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVINS.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT COMPOSITION. INHIBINS APPEAR TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3:939-948(1989).
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Best Local
     ■ Mason
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DISULFID
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CARBOHYD
CONFLICT
                                                                                                                         IHBB_PIG STANDARD; PRT; 349 AA. P04088; 01-NOV-1986 (Rel. 03, Created) 01-NOV-1986 (Rel. 03, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 17thlbin beta B chain precursor (Activin beta-B chain) (Fragment).
            SEQUENCE FROM N.A.
TISSUE=Ovarian follicular fluid;
MEDLINE=86092207; PubMed=2417121;
                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00671; INHIBINBB.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                      Sus scrofa (Pig).
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InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                           V--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                   TGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                               FFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGT
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                                                                                                                                                                                                                                                                                                                                                                                      LVPESQVAHSSLILGWF-----SHRPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NATQTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------DQRQEEYEIISFADTDLSSINOTRLEFHFSGRMASGMEVRQTRFMFFVQ-FPH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRVDGDFLEAVKRHILSRLØMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR-GPRRE---TLLEH-- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACLLLLAAGWLGPEAWGSPTPPPTPAAPPPPPPPPGSPGGSQDTCTSCGG----FRRPEEL 67
   Ą.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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407 AA;
   Hayflick J.S.,
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407
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                                                                           Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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BY SIMILARITY.
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BY SIMILARITY.
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S -> A (IN REF. 2)
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 Esch F.,
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Ueno N., Ying
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                                                                            Euteleostomi;
Sus.
S. -Y.,
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Pfam; PF00688; TGFb_propeptide;
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Isolation and characterization of native activin B.";

J. Biol. Chem. 267:16385-16389(1992)

-I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00204; TGFB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
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InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92355604; PubMed=1644823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 318:659-663(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor structure and homology with transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guillemin R., Niall H., Seeburg P.H.; "Complementary DNA sequences of ovarian follicular fluid inhibin
        146
                                                                77
                                                                                                                  91
                                                                                                                                                                          17
                                                                                                                                                                                                                             44 LDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLR-GPRRE---TLLEH-----
                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X03267; CAA27021.1; -.
A01394; WFPGBB.
P18075; IBMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVINS.
SUBUNIT: DIMERIC, LINKED BY ONE
QTMNIRVLVLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQV
                                                                                         DQRQEEYEIISFADTDLSSINOTRLEFHFSGRMASGMEVRQTRFMFFVQ-FPH----NAT | :: | :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: : |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: :: |: : |: :: |: :: |: : : |: : |: : |: : : |: : |: : : |: 
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                                                       DGQERVSEIISFAETDGLASSRVRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSR
                                                                                                                                                                     LEAVKRHILNRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor;
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00250; TGF_BETA_1; 1.
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349
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246
314
348
313
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                                                                                                                                                                                                                                                                                                                 29.5%;
35.8%;
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                                                                                                                                                                                                                                                                                                                                                                                      INHIBIN BETA B CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
IN-LINKED (GLCNAC. . .) (POTE)
WY: C571EA91ADA5DE77 CRC64;
                                                                                                                                                                                                                                                                                                                 Score 546;
Pred. No. 2.
                                                                                                                                                                                                                                                                                     Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR MORE DISULFIDE
                                                                                                                                                                                                                                                                                                                                          DΒ
                                                                                                                                                                                                                                                                                                           7e-43;
                                                                                                                                                                                                                                                                                                                                    Length 349;
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-I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, J. BIO1. Chem. 267:16385-16389(1992).

-I- FUNCTIVELY, THE SECRETION FOLLITROPIN BY THE PITUITARY GLAND. INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y., Guillemin R., Niall H., Seeburg P.H.; "Complementary DNA sequences of ovarian follicular fluid inhibin show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Follicular fluid;
MEDLINE=86092207; PubMed=2417121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1986 (Rel. 02, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta A chain precursor (Activin beta-A chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P03970;
23-OCT-1986 (Rel. 02, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor structure and homology with transforming growth
                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
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                        EMBL; X03266; CAA27020.1; *.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSUE-Follicular fluid
                                                                                                                                                                                                                                         SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE ACTIVINS
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.

ACTIVIN A IS A HOMODIMER OF BETA-B.

ACTIVIN B IS A HOMODIMER OF BETA-B.

ACTIVIN AB IS A DIMER OF BETA-B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGWSDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTV--NSCC
                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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A01393; WFPGBA

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     SSSEEPPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
IHBA_HUMAN
P08476; 014599;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1nhibin beta A chain precursor (Activin beta-A chain) (Erythroid inhibin beta A chain protein) (EDF).
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DISULFID
DISULFID
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pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
ProDom; PD000357; TGF-beta; 1.
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InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                 ASFHTAVLNILKANAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLASCWIIVRSSPTPGSGGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                       CEQCHETGASLVLLGKKKKKEEEAEGRKRDGEGAGVDEEKEQSHRPFLMLQARQSEEHPH
                                                                                                                                                                                                                                                                                                                                                                                      GSADAGEEAEDVGFPEEKSEVLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSALDIRTA
                                                                                                                                                                                                                                                                                                                                                              SQVAH----SSLILG------VEGKH
                                                                                                                                                                                                                                                                                                                                                                                                               -----VLRPYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVELEDDIGRRAEM---NELMEQTSEIITF
                                                                                                                                                                                  so-
                                                                                                                                                                                                                                                                                     RRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS
                                                                                                                                                                                                                                                                                                            RVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGNPGIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADTDLSSINQTRLEFHFSGRMASGMEVRQTRFMFFVQFPH-NATQT-MNIRVL-----
                                                                                                                                                                                   424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 AA;
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312
319
348
352
388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone; Glycoprotein; Signal
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424
424
320
389
421
423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47476 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 543; DB 1;
Pred. No. 6.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (P
436BC62226FDAF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHIBIN BETA A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 424;
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                                                 EMBL; M13436; AAA59168.1; -
EMBL; X04447; CAA28041.1; -
EMBL; X57578; CAA40805.1; JOINED.
EMBL; X57579; CAA40806.1; -
EMBL; X57579; CAA40806.1; -
EMBL; AC005027; AAD43185.1; -
EMBL; AC005027; AAD43185.1; -
EMBL; AC0428; CAA35767.1; -
EMBL; A14422; CAA0119.1; -
EMBL; X72498; CAA51163.1; -
                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glossip D., Dubuque T., Graves T., Submitted (JUN-1998) to the EMBL/Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92135888; PubMed=1777673;
Tanimoto K., Handa S.I., Ueno N.,
"Structure and sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.; "Erythroid differentiation factor is encoded by the same mRNA as that of the inhibin beta A chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 311-426 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87005283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the inhibin beta A chain.";
Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mason A.J., Niall H.D., "Structure of two human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 311-426 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Seq. 2:103-110(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88190086; PubMed-3267209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 135:957-964(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-86186863; PubMed-3754442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILLIAM (MAY-1993) to the EMBL/GenBank/DDBJ databases.

FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

ERYTHROID DIFFERENTIATION, INSULIN SECRETION, MERVE CELL SURVIVAL,

EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR

THISTORY OF THE PROPERTY OF THE PROPERTY OF THEIR

THEIR THE PROPERTY OF THE PROPER
                A30884; A30884.
B24248; B24248.
                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: DIMERIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H., Walter M., Northemann W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=3758355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.D., Seeburg P.H.;
human ovarian inhibing,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINKED BY ONE OR MORE DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
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of the human activin be
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IHBA_MOUSE
Q04998;
01-FEB-1994 (
01-FEB-1994 (
16-OCT-2001 (
Inhibin beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                            424
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Matches 132;
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PIR; S30488; S30488.
HSSP; P18075; 1BMP.
MIM; 147290; -.
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CONFLICT
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DISULFID
DISULFID
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Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
                                                            364 SSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEEC
                                                                                            290 ISASEHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMYVEAC
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SMART; SM00204; TGFB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR002400; GF_cyskr
InterPro: IPR000491; Inhibin_
InterPro: IPR001839; TGF-beta
InterPro: IPR001111; TGFb_N.
                                 350 GCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LLASCWITYRSSPTPGSEGHSAAPDCPSCALAALPKDYPNSQPEMYEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LLALLFLTPTTVVNPKTEG-----PCPACWGAIF--DLESQRELLLDLAKKSILDKLHLS 58
                                                                                                                                                          KHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHYAGMPG
                                                                                                                                                                                                         CEQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDH
                                                                                                                                                                                                                                         VPESQVAHSSLIL-----VEG
                                                                                                                                   PHRRRRGLECOGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG
                                                                                                                                                                                                                                                                            GSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDVRIA
                                                                                                                                                                                                                                                                                                                                              AE---SGTARKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQ 183
                                                                                                                                                                                                                                                                                                                                                                                ADTDLSSINGTRLEFHESGRMASGMEVRQTREMEFVQFPH-NATQT-MNIRVLVLRPY-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                   KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEM -- - NELMEQTSEIITF 126
                                                                                                                                                                                                                                                                                                              Similarity
426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hormone; Glycoprotein; Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGF-beta; 1.
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310
426
322
391
423
423
425
165
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; Inhibin_betaA.
; TGF-beta.
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BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201CDEDF99CB6919 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                   363
                                                                                                                                                                     289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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(Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 40, Last annotation update)

STANDARD;

PRT;

424 AA

chain precursor (Activin beta-A chain).

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SOCCEPT THE TRANSPORT OF THE THE TRANSP
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                                                                                                                                      Query Match
Best Local :
                                                                                                                Matches
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Development 117:711-723(1993).

-I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

-I- FUNCTION: THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00438; GFCYSKNOT. PRINTS; PR00670; INHIBINBA. ProDom; PD000357; TGF-beta; 1.
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                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00019; TGF-beta; 1. Pfam; PF00688; TGFb_propeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR: S31440: S31440.
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                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001839; TGF-beta. InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002400; GF_cysknot.
InterPro; IPR000491; Inhibin_betaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:96570; Inhba
  10
                                                        Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBIN A IS A DIMER OF ALPHA AND BETA-A. INHIBIN B IS A DIMER OF ALPHA AND BETA-B. ACTIVIN A IS A HOMODIMER OF BETA-B.

ACTIVIN B IS A HOMODIMER OF BETA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVA EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B
  LLASCWIIVRSSPTPGSEGHGSAPDCPSC--ALATLPKDGPNSQPE-MVEAVKKHILNML 66
                                                        LLALLFLTPTTVVNPKTEG-----PCPACWGAIFDL-----ESQRELLLDLAKKSILDKL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00204; TGFB; 1
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGF_BETA_1; 1.
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424
320
389
421
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                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                   Score 538;
Pred. No. 1
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; 80C251B8754A7213 CRC64,
                                                                                                                                                                                                                                                                             INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBIN BETA A CHAIN.
                                                                                                                Mismatches
                                                                                                                                   DB 1;
.9e-42;
                                                                                                                                                               Length 424;
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RESULT 14
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P18331;
                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complementary deoxyribonucleic acids and expression Mol. Endocrinol, 1:561-568(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.; "Rat inhibin: molecular cloning of alpha- and beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibin beta A chain precursor (Activin beta-A chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91042598; PubMed=3153478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158
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                                                                                                                                                 ACTIVINS.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
                                                                                                                                                                                                                                                                                                                                                                                                 RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
                                                                                                                                                                                                                                                                                                                                    GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEE
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                                                                                                                                                                                                                                                                                                                      OPPOSE
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Best Local
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Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                      01-OCT-1996
01-OCT-1996
16-OCT-2001
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DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
INHBA ..
         Inhibin beta
                                                       IHBA_HORSE
P55102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002400; GF_cysknot.
InterPro; IPR000491; Inhibin_betaA.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
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                                                                                                                           CGCS 424
                                                                                                                                                CGCS 352
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                                                                                                                                                                                          GISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEA
                                                                                                                                                                                                                 HPHRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTS
                                                                                                                                                                                                                                    GKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMP
                                                                                                                                                                                                                                                            RIACEQCQESGASLVLLGKKKKKEVDGDGKKKDGSDGGLEEEKEQSHRPFLMLQARQSED
                                                                                                                                                                                                                                                                                 HPQGSLDMGDEAEEMGLKGERSELLLSEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDV
                                                                                                                                                                                                                                                                                                                                                                                                    HLKKRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEM---NELMEQTSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLALLFLTPTTVVNPKTEG-----PCPACWGAIFDL----ESQRELLLDLAKKSILDKL 55
                                                                                                                                                                                                                                                                                                                                                      ITFAE---SGTARKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQK 180
                                                                                                                                                                                                                                                                                                                                                                           ISFADTDLSSINGTRLEFHESGRMASGMEVRQTREMEFYQFPH-NATQT-MNIRVLVLRP 157
                                                                                                                                                                                                                                                                                                                                                                                                                         LLASCWIIVRSSPTPGSEGHGAAPDCPSC--ALATLPKDGPNSQPE-MVEAVKKHILNML 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
    (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
a A chain precursor (Activin beta-A chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                ------DTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165
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                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hormone; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308
424
424
421
423
165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.1%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHIBIN BETA A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 538;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (P
B2DAF7917FA50984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (BY SIMILARITY)
                                                                  426
                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                     420
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THE THE TRANSPORT OF TH
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DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002400; GF_cysknot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D50326; BAA08862.1; -. HSSP; P18075; 1BMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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[1]
                                                                                                                                                                                                           Local
     59
                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF BETA-A.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEIL MED. Sci. 57:469-473(1995).

FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE

FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

ERVITHROID DIFFERENTIATION, INSULIN SECRETION, DEPENDING ON THEIR

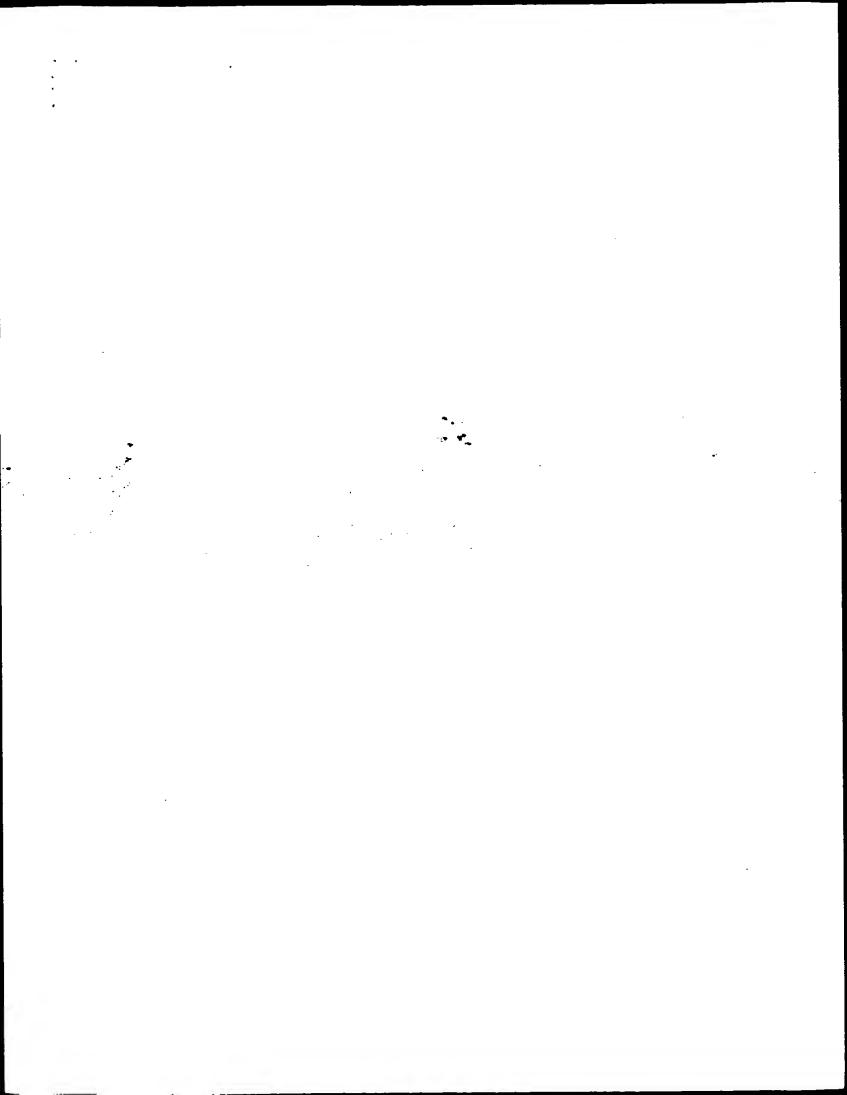
EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR

SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
     QRPILSRPVSRGALKTALQRLR------
                                                          LLASCWIIVKSSPTPGSEGHSAAPNCPSCALATLPKDVPNAQPEMVEAVKKHILNMLHLK 69
                                                                                                                 LLALLFLTPTTVVNPKTEG-----PCPACWGAIF--DLESQRELLLDLAKKSILDKLHLS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor;
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000491; Inhibin_betaA.
IPR001839; TGF-beta.
IPR0011111; TGFb_N.
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hormone; Glycoprotein; Signal.
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426
322
391
423
423
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                                                                                                                                                                                                        28.98;
31.28;
                                                                                                                                                                                                                                                                                             MW;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO
; E481060B8368A77D CRC64;
                                                                                                                                                                                                     Score 534; DB 1;
Pred. No. 4.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                        Mismatches
-GPRRETLLEHDQRQEEYEIISF 102
                                                                                                                                                                                                                             Length 426;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                           82;
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Job t	ф	Ωy	멍	Ş	дb	γ	망	Q	망	οy	망	γO	д
h con	424	350	364	290	304	230	244	203	184	159	127	103	70
Search completed: October 12, 2002, 02:06:56	424 GCS 426	GCS 352	SSLSFHSTVINQYRLRGHNPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEEC 423	ISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEAC	PHRRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG 363	KHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPG	244 CDOCHETGASLVLLGKKKKKEEEGEGKKKDGGEAGAGVDEEKEQSHRPFLMLQARQSEDH 303		184 GSSDTREEAEEADLMEERSEQLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDIRIA 243		127 AESGTARKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRSKVTIRLLQQQKHPQ 183	ADTDLSSINGTRLEFHFSGRMASGMEVROTREMEFVQFPH-NATQT-MNIRVLVLRPY 158	70 KRPDVTQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITF 126
	مسار	\$	123	349	363	289	303	229	243 ·	202.	183	158	126

Job time : 15.5 secs



GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Result
                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein • protein search, using sw model
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112
113
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116
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             Score
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1850
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112:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
   SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                               sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_unclassified:*
sp_rvirus:*
sp_truirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                           sp_phage:*
sp_plant:*
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                                                                                                                                                    Length DB
   6613113
  ID
                                                                                                               Q91696
Q91XH3
Q91350
                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search time 42 Seconds (without alignments)
1449.862 Million cell updates/sec
                        Oghbp0 homo saplen
Og0261 brachydanio
Og0860 cynops pyrr
OgpwrB carassius a
Og085p9 meleagris g
Ogpw65 carassius a
Og5kp1 ailurus ful.
O42125 pagrus majo
Og5hp3 ailurupoda
Q95kp2 ursus malay
Q9w6t9 brachydanio
Q9dgfl cyprinus ca
                                                                                                             Q91696 xenopus lae
Q91xh3 mus musculu
Q91350 xenopus lae
                                                                                                                                                  Description
                                                                                                      Q9pwg6 anguilla ja
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45	4.4	43	2	41	40	39	38	37	36	35	ω 4-	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
283	283.5	285	286	287	288	295.5	300.5	306.5	309.5	310	313.5	314.5	317	318	321	322	322.5	324.5	325	330.5	331	331.5	331.5	334	341	350	356	356
15.3	15.3	•	•	•	15.6	16.0	16.2	16.6	16.7	•	16.9	17.0	17.1	17.2	17.4	17.4	17.4	17.5	17.6			17.9	17.9	18.1	18.4	18.9		19.2
375	373	102	375	586	375	102	389	102	102	373	385	376	377	373	120	373	104	373	373	376	115	376	376	115	115	115	115	115
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Q95N97	061643	Q90390	Q95J86	Q9VQG9	Q9GM97	Q9DET3	Q90YY0	Q90389	Q90388	Q98UB3	Q90W05	Q98TB4	Q98TB3	Q9DD18	Q9W6T8	Q90ZD2	Q98861	Q90ZD1	Q90W17	090W06	Q9DGE8	80M060	Q90WC9	Q9DGF2	Q9DGE7	Q9DGF0	Q9DGE6	Q9DGE9
	rosophila	090390 carassius a	095186 macaca fasc	Q9vqq9 drosophila	O	oncorhynch	ictalurus	carassius								-				umbrina	oryzias		morone sa	SO.	oryzias l	cyprinus	oryzias l	Q9dge9 cyprinus ca

ALIGNMENTS

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Q91696
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
 Query Match
                                       InterPro; IPR002400; GF_cysknot.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRODOM; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE: PS00250; TGF_BETA; 1.
Glycoprotein; Signal.
SIGNAL 253 POTEK
CHAIN 254 367 'ACTI
                                                                                                                                                                                                                                                                                                                                                                     Q91696 PRELIMINARY;
Q91696;
Q91696;
Q1-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-DEC-2001 (TrEMBLrel. 19, L
ACTIVIN D PRECURSOR.
                         SEQUENCE
                                                                                                                                                                                                  EMBL; D49543; BAA08494.1; HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                             TISSUE-LIVER;
MEDLINE-95275314; PubMed-7755637;
                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID-8355,
                       254
367 AA;
                                   253
367
                   253 POTENTIAL.
367 'ACTIVIN D'.
41729 MW; C7E6334BD606FA04 CRC64;
 37.8%;
                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Score 699.5;
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DB 13; Length 367;
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RESULT 2
Q91XH3
ID Q91XH
AC Q91X
AC Q91X
DT 01-D
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                                                                                                                                                                                                                                                                                                                                          Matches 141;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                          ,
                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010404; AAH10404.1; -. SEQUENCE 350 AA; 39002 MW; 9B7EA8AFFAC389FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91XH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91XH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBIN BETA E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 MVVEACGCS 352
226 RVE--GKHRVRRRGIDCOGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLH 283
                                     164 TSSGWHALTLPSSGLRSEDSGVVKLQLEFRPLDLNSTAAGLPRLLLDTAGQQRPFLELKI
                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 VAGMPGISASEHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AKVHEQSHHATKRSLNCDQNSNLCCRKDYYVDFKDIGWNDWIIKPEGYQINYCMGLCPMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 RLEFHFSGRMASGMEVROTRFMFFVOFPHNATQTMNIRVLVLRPYDTNLTLTSOYVVQVN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 LLTLLGALAASTQGLTKKSQCPSCG-----VQDKEVMIELAKQQILQKLHLKERPNITH 67
                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                12 LLWALVWV------QSTRSACPSCGGPTLAPQGERALVLELAKQQILEGLHLTSRPRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                    5 LLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILS
                                                                         NASGWYOLLLGPEAQAACSOGHLTLEL-----VPESQVAHSSLILGWF-SHRPFVAAQV 225
                                                                                                                FQLSPLWSHHL----YHARLWLHVPPSFPGTLYLR--IFRCGTTRCRGFRTFLAEH--QT 163
                                                                                                                                                  FHFSGRMASGMEVRQTRFMFFVQFPHNATQTMNIRVLVLRPYDTNL----TLTSQYVVQV \overset{\circ}{172}
                                                                                                                                                                                                                         RPVSRGALKTALQRLRGPR-----RETLLEHDQRQEEYEIISFAD--TDLSSINQTRLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIVEACGCS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAGAPGMAASFHTTVLNLIKANNI--QTAVNSCCVPTKRRPLSMLYFDRNNNVLKTDIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLH 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTGWOTFSLKSMLOTFFDGGNKSLQLELNCDGCQDVPVLANPNN-----SHQPFLVAQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASGWYQLLLGPEAQAACSQGHLTLEL------VPESQVAHSSLILGWFSHRPFVAAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLNFQFTRDKEQSAHVLQAHLWLFFKANRTSQQNETIRLYLVQEAYSRRILISEKLIEPR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVSRGALKTALQR--LRGPRRETLL-----EHDQRQEEYEIISFADTDLSSINQT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSR 65
                                                                                                                                                                                       RPLPQAALTRALRRLQ-PKSMVPGNRE------KVISFATIIDKSTSTYRSMLT 1,11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145;
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.38;
                                                                                                                                                                                                                                                                                                                                                         31.8%; Score 587.5; DB 1 38.0%; Pred. No. 1.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                                                                                          66; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.1e-61;
5; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350
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                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Gaps
                                                                                                                                                                                                                                                                                                                                          55;
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                          14;
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Q91350
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91350 PRELIMINARY; PRT; 3:
Q91350;
Q91350;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequential C1-DEC-2001 (TrEMBLrel. 19, Last annot ACTIVIN BETA B SUBUNIT.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002400; GF_cysknot.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
Pfam; PF00618; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1
PRINTS; PR00438; GFCYSKNOT.
PrODOM; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS00250; TGF_BETA; 1.
Glycoprotein.
SEQUENCE 370 AA; 41679 MW; AD21502AC45F1DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S61773; AAB26863.1; HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-93273083; PubMed-8500654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. Biol. 157:474-483(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dohrmann C.E., Hemmati-Brivanlou A., Thomsen G.H., Fields Woolf T.M., Melton D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·!- SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression of activin mRNA during early development in Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
                                     238
                                                                                                                                                      166
                                                                                                                                                                                         118
                                                                                                                                                                                                                             109
                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                          4 LLLPLLLAGLARTCAPSPTPEPGCPSCHP---PMEPE---MLEAVKRHILTLLHMQDRPN 57
                                                                                                                                                                                                                                                                                                                                                                             5 LILLALLE -- LTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAGMPGISASFHTAVLNLLKANA--AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCPLHVAGMPGISASFHTAVLNLLKANAA-AGTTGRGSCCVPTSRRPLSLLYYDRDSNIV
                                                                                                                                                                                                                             SINOTRLEFHESGRMASGMEVROTREMETVQFPH---NATQTMNIRVLVLRPYDTNLTLT 165
                                                                                                                                                                                                                                                                                                    LSRPVSRGALKTALQRLRGPR-RE-----TLLEHD-----QRQEEYEIISFADTDLS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDMVVEACGCS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAGSPGIAASFHSAVESLLKANNPWPAGS----SCCVPTARRPLSLLYLDHNGNVVKTDV 339
                                                                                                                  VEKKYDIRRSGWHTFPLTEAIQSLFEEGERRLNLEVQCDGCGEYSVIPVYVDPGEESHRP
                                                                                                                                                                                       TASRVRLSFTIANEGNQNLFVFQSNLWLYLKLPEVMDKSRRKIRIKVHFQDAFNPDKMNM 177
                                                            FVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTG
                                       FLVVHARLADNKHRIRKRGLECDGHTNLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEG
                                                                                                                                                    SQYVVQVNASGWYQLLLGPEAQAACSQG--HLTLELVPESQVAHSSLIL----GWFSHRP
                                                                                                                                                                                                                                                                  ITHMVPRAAMVSALRKLHAGRVREDGNLEIPDLDGHSLPPPGHSTENSAEIITFAETDDV 117
                                                                                                                                                                                                                                                                                                                                                                                                                   130;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  30.6%; Score 566.5; DB 1 34.7%; Pred. No. 2.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
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                                                                                                                                                                                                                                                                                                                                                 Matches 121;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO01381; Inhibin_betaB.
InterPro; IPRO01318; Inhibin_betaC.
InterPro; IPRO01318; Inhibin_betaC.
InterPro; IPRO01839; TGF-beta.
InterPro; IPRO01111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF0068B; TGFb_propeptide; 1.
Pfam; PF0068B; TGFb_propeptide; 1.
PRINTS; PR00671; INHIBINBC.
PRINTS; PR00672; INHIBINBC.
PRODOm; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anguilla japonica (Japanese eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillioidei;
Anguillidae; Anguilla.
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-TESTIS;
                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-7937
                                                                                                                    201
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                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                      72 LKTALQRLR-GPRRE------TLLEHDQRQEEYEIISFADTDLSSINQTRLEFH 118
                                                                                                                                                                                                                                                                                                             14 PTTVVNPKTEGPCPACWGAIFDLESQRELL--LDLAKKSILDKLHLSQRPILSRPVSRGA 71
                                                                                                                                                                                                                                                                                          24
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                             MVTALRKLHAGKVREDGRVEIPNLDGHATYNNEVQEDTSEIISFAESD--ELTSSKSSFH 140
                                                                                                                                                                      FLISNEGNONLYVSQASLWLYFRLLPSASEKGSRRKVTVKVYYQQTGAAAAAAAAAGGRW 200
                                                                                                               GLVEKRVELKRSGWHTFPLTEPYRGVFERGDRRQDLDVRCEGCEAAAVLPVLVDPGDESH
EGSCPAYMAGVPSSASSFHTAVVNQYRMRGMS-PGSMNSCCIPTRLSTMSMLYFDDEYNI 379
                          TGQCPLHYAGMPGISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNI 336
                                                       RPFLVVQARLADGKHRIRKRGLECDGTGGLCCRQQFYIDFRLIGWNDWIIAPSGYFGNYC
                                                                       RPFVAAQVRV-EGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFC 276
                                                                                                                                                                                               F*-SGRMASGMEVRQTREMEFYQFPHNATQTMNIRVLVLRPY--DTNLTLTS----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGTETQTVSQDTCASC-GLGQPEESGRMDIDFLEAVKRHILNRLQMRERPNITHPIPKAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRDVPNMIVDECGCA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTDIPDMVVEACGCS 352
                                                                                                                                         -QYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQVAHSSLIL-----GWFSH 217
                                                                                                                                                                                                                                                                                                                                                                                                      395 AA; 43889 MW; FA56DD62D18509A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          29.5%; Score 545.5; DB 13; Length 32.2%; Pred. No. 3.5e-46;
                                                                                                                                                                                                                                                                                                                                          78; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395
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                                                                                                                                                                                                                                                                                                                                                                          395;
                                                                                                                                                                                                                                                                                                                                             41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00669; INHIBINBA.
PRINTS; PR00670; INHIBINBA.
PRINTS; PR00672; INHIBINBC.
PrODOM; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA; 1.
Glycoprotein; Hypothetical protein.
Glycoprotein; Hypothetical protein.
SEQUENCE 426 AA; 47454 MW; 339276317BD5B408 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases - STMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL, AF218018; AAG17260.1; -.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9HBPO;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR000491; Inhibin_betaA.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gu J.R., Wan D.F., Zhao X.T., Zhou X.M.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL 47.5 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu J., Han L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Novel Human cDNA clones with function of inhibiting cancer cell
                                                                                                244 CEQCQESGASLVILIGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDH
                                                                                                                                                                      184
                                                                                                                                                                                                                                     127
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                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                             10 LLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                 ISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMYVEAC
                                                 KHRVRRRGIDCQGGSRMCCRQEFEVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPG
                                                                                                                                VPESQVAHSSLIL------VEG
                                                                                                                                                                                                                              AE---SGTARKTLHFEISKEGSDLSVVERAEVWLFLKVPKANRTRTKVTIRLFQQQKHPQ
                                                                                                                                                                                                                                                                                                                             PHRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSG
                                                                                                                                                               GSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDVRIA
                                                                                                                                                                                                                                                            ADTDLSSINGTRLEFHFSGRMASGMEVRQTRFMFFVQFPH-NATQT-MNIRVLVLRPY-- 158
                                                                                                                                                                                                                                                                                               KRPDVIQPVPKAALLNAIRKLHVGKVGENGYVEIEDDIGRRAEM···NELMEQTSEIITF
                                                                                                                                                                                               VKRDVPNMIVEECGCA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                              29.0%; Score 537; DB 4; Length 426; 31.2%; Pred. No. 2.7e-45; Live 69; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               He L.P., Li H.N., Yu Y.
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Interpro; IPR001839; TGF-beta.
Interpro; IPR001811; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PD000137; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (2ebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X76051; CAA53636.1; -. HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Disruption at mesoderm and axis formation in fish by ectopic expression of activin variants: the role of maternal activin. Genes Dev. 8:1448-1462(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZFIN; ZDB-GENE-990415-2; inhbb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wittbrodt J., Frederic R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95011555; PubMed=7926744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHBB OR ZACTBETAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVIN BETA B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
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                                                      267 QPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANA-AAGTTGRGSCCVPTSRRPL 325
                                                                                                                   249 LVDPSDPSHRPFLVVRAQQADGKHRIRKRGLECDGNNGGLCCRQQFYIDFRLIGWNDWII
                                                                                                                                                                                                                                                                                               163 TLTSQYV-----VOVNASGWYQLLLGPEAQAACSQGHLTLELVPESQVAHSSLILGW
                                                                                                                                                                                                                                                                                                                                                                                                                        105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSQRPILSRPVSRGALKTALQRLRG-------PRRETLLEHDQRQEE-YEIISFAD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCS 352
APAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQYRMRGMSPGSV--NSCCIPTKLSTM 366
                                                                                                                                                                                                                                         ---GONVHWPMMEKRVELKRSGWHTFPVSEAIREMLAKGGRRQDLDIHCEGCEAANVLPI 248
                                                                                                                                                                                                                                                                                                                                                               SDDVTPSKSSLYFLISNEGNQNLYVLQANLWLYFKLMPGTLEKGLRAKVTVRVHSYEPG- 191
                                                                                                                                                                                                                                                                                                                                                                                                                     TDLSSINGTRLEFHFSGRMASGMEVROTR-FMFFVQFPHNATQTMNIRVLV-LRPYDTNL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRERPNITHPIPKAAMVTALRKLHAGKVREDGRVEIPNLDGHAAHNEVQEETSEIISFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSVTCLMACLLSVQCSSLGAETGSQESQCVSCGLGHQEDSGRMDTDFLEAVKRHILNRLQ 72
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5 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 AA; 43830 MW; FA769C4D9BE4D252 CRC64;
                                                                                                                                                    -SHRPFVAAQV-RVEGKHRVRRRGIDCQGGS-RMCCRQEFFVDFREIGWNDWII 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 83; Mismatches 139;
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Last annotation update)
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Best Local :
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Pfam; PF00688; TGFb_propeptide; 1
PF1NTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O98860; PRELIMINARY;
Q98860;
01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein.
SEQUENCE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000491; Inhibin_betaA.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 testis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto T., Nakayama Y., Abe S.; "Expression of activin beta subunit genes in sertoli cells of newt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96295508; PubMed=8702409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002400; GF_cysknot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 SLLYYDRDSNIVKTDIPDMVVEACGCS 352
354
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                              293
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                                                                                                                                                                                                                                                                                                                                                                                   10 LLLGLCWIATRASPTPGTEGQGSVTDCPSC--ALGRLEKAAPSSQADMVEAVKKHILSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 5 LLLALLFLTPTTVVNPKTEG-----PCPACWGAIFDLE----SQRELLLDLAKKSILDKL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMLYFDDEYNIVKRDVPNMIVEECGCA 393
                         SEHTAVLNILKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                            RKKRGLECDGKVSICCKKQFYVSFKDIGWSDWVIAPPGYTANYCEGDCPMYITGTSGSGP
                                                                                            VRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISA
                                                                                                                                                                                        IRLYQQQQRGQDEERGQERDKKEVLIAEKTLDTKRSGWHTFNIAKSIQHLLDQGKTSLDI
                                                                                                                                                                                                                          LRPY-----
                                                                                                                                                                                                                                                      EIITFAEA-----GQSKKVLHFEISKEGSDLSLVEQAEFWLFVKLNKSNRSRTK----LT
                                                                                                                                                                                                                                                                                      EIISFADTDLSSINQTRLEFHFS-GRMASGME-VRQTRFMFFVQF-PHNATQTMNIRVLV 154
                                                                                                                                                                                                                                                                                                                      HMRSRPNITQPVPKAALLNAIKKLHVGKVGQDGYVEIEDDVGRRAERSELLE-----QTS
                                                                                                                                                                                                                                                                                                                                                   HLSQRPILSRPVSRGALKTALQRL-------RGPRRETLLEHDQRQEEY 97
 SFHAAVINQYRMRGYSPFTSVKSCCVPTKLRAMSMLYYDDGQNIIKKDIQNMVVEECGCS
                                                                                                                          RIACDQCQETGATPTLLGKKKKKEEEVKAANGSAGDEEREQSHRPFLMIMARQSEEHPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 AA; 46303 MW; 46F66D112AA1B010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.5%;
                                                                                                                                                        ----VPESQVAHSSLILG----WFSHRPF--VAAQVRVEGKHR
                                                                                                                                                                                                                        -DTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLEL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.18-44, 3; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 528; DB 13;
Pred. No. 2.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224:451-456(1996).
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Best Local S
Matches 120
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InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001318; Inhibin_betaC.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
InterPro; IPR001111; TGFb_N.
InterPro; IPR001111; TGF-beta; 1.
InterPro; IPR0011; INTERINBB.
INTERPROSCO: INHIBINBC.
INTERPROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carassius auratus (Goldfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Carassius.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACTIVIN BETA B SUBURTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PWR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PWR8;
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391
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ბ :: წ
                                                                                                                                                                                                         LLLGPEAQAACSQGHLTLELVPESQVAHSSLILLGWF-----SHRPFVAAQV-RVEGKHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGPCPAC-WGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLRG
                                                                                                                  ASFHTAVLNLLKANA·AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACG
                                                                                                                                                                                                                                                                             FPVSEAVREMLAKGGRRQDLDIHCEGCEAANVLPILVDPSDPSHRPFLVVRAQQADSKHR
                                                                                                                                                                                                                                                                                                                                                                                                    ROTR-FMFFVQFPHNATQTMNIRVLV-LRPYDTNLTLTSQYV------VQVNASGWYQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKVREDGRVEIPNFDGHAAHNEVQEETSEIISFAESDDVTPSKSSLYFLISNEGNQNLYV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRKRGLECDGTNGGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCPAYMAGYPGSA
                                                                                                                                                                                                                                                                                                                                                                      LQANLWLYFKLLPGTQEKGLRRKVTVRVRSYEPG----GQNVHWPMMEKRVELKRSGWHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESQCASCGLGHPDDSGRMDTDFLEAVKRHILNRLOMRERPNITHPIPKAAMVTALRKLHA 96
                                                                                      SSFHTAVVNQYRMRGISPGSV--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECG
392
                                            352
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277 392 A
392 AA; 43853 MW;
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ACTIVIN BETA B SUBUNIT.
; 73AAA7E1C0B2450B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 9
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InterPro; IPR00111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1
PRINTS; PR00669; INHIBINA.
PRINTS; PR00670; INHIBINBA.
PRINTS; PR00672; INHIBINBC.
PRINTS; PR00672; INHIBINBC.
PRODOm; PD000357; TGF-beta; 1.
SMARP; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ahn J., You S., Kim H., Foster D.N., El Halawani M.E.;

"Molecular cloning of turkey inhibin-alpha and betaA subunits.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL; AF336338; AAK21265.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meleagris gallopavo (Common turkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00250; TGF_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002405; Inhibin_alpha.
  367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLVICWIIVRSSPTPGSEGHSSVTDCPSCALTTLSKDVPSSQPEMVEAVKKHILNMLHLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRPILSRPVSRGALKTALQRLR----GPRRETLLEHDQR-----QEEYEIISFADT 105
                                                   HTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                              COETGASLVLLGKKKKKEDDGEGKEKDAGELTGEEEKEOSHRPFLMMLARHSEDRQHRRR
                                                                                                                                             RRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SGTPKKTLHFEISKEGSELSVVEHAEVWLFLKVSKANRSRTKVTIRLFQQQRQPKGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLSSINQTRLEFHFS--GRMASGMEVRQTRFMFFVQFPHNATQTMNIRVLVLRPY----
HSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS
                                                                                                          KRGLECDGKVNICCKKQFFVSFKDIGWSDWIIAPTGYHANYCEGECPSHIAGTSGSSLSF
                                                                                                                                                                                                                                                                                                                                           EGSEDMEDGGLKGERSETLISEKAVDTRKSTWHIFPVSSSVQRLLDQGKSSLDVRIACDL
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127; Conserv
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IPR001318; Inhibin_betaC
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                                                                                                                                                                                                                                                                                                                                                                                                     DTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLEL---VPE
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Pred. No. 1.8e-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 152;
                                                                                                                                                                                                                                                                -GWF-----SHRPFVAAQVR--VEGKHRVR
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424
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RESULT 10

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RESULT 11
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotatic
ACTIVIN BETA A PRECURSOR.
Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vo
Actinopterygii, Neopterygii; Teleostei; El
Cypriniformes; Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1
PRINTS; PR00669; INHIBINA.
PRINTS; PR00670; INHIBINBA.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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InterPro; IPR000491; Inhibin_betaA.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                          MIVEECGCS
                                                                                MVVEACGCS
                                                                                                                    VAGMPGISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPD
                                                                                                                                                     KPAEEHPHRRSKRGLECDGKIRVCCKRQFYVNFKDIGWSDWIIAPSGYHANYCEGDCPSH
                                                                                                                                                                   QVRVEGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLH
                                                                                                                                                                                                                           GPEAQA-----
                                                                                                                                                                                                                                                  QANVWLLLKVAKGSRGKGKVSVQLLQHGKADPGSADGPQEAVVSEKTVDTRRSGWHTLPV
                                                                                                                                                                                                                                                                                              VGEDGTVEMEEDGGGLGEHREQSEEQPFEIITFAEPGDAPDI--MKFDISMEGNTLSVVE
                                                                                                                                                                                                                                                                                                                    ------RETLLEHDQRQEE--YEIISFADT-DLSSINQTRLEFHFSGRMASGME 128
                                                                                                                                                                                                                                                                                                                                                                   PCPACWGAIFDLESQREL-LLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQRLRGPR
                                                                                                                                                                                                  SRTVQTLLDGDSSMLSLRVSCPMCAEAGAVPILVPTESNKGKER----EQSHRPFLMVVL
                                                                                                                                                                                                                                                                       VRQTRFMFFVQFPHNATQTMNIRVLVLRPYDTNL----TLTSQYVVQVNASGWYQLLL 182
                                                                                                                                                                                                                                                                                                                                             PCPSCALAQRQKDSEEQTDMVEAVKRHILNMLHLNTRPNVTHPVPRAALLNAIRRLHVGR 101
                                                                                                                                                                                                                                                                                                                                                                                            hal Similarity
                                                                                                       VASITGSALSFHSTVINHYRMRGYSPFNNIKSCCVPTRLRAMSMLYYNEEQKIIKKDIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                          289
404 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
 PRELIMINARY;
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                                                          404
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                                                                                                                                                                                                                                                                                                                                                                                                                                         44799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   26.48;
32.28;
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                                                                                                                                                                                                                         ---ACSQGHLTLELVP-ESQVAHSSLILGWFSHRPF--VAA
                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.9e-40;
1; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 488.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
ACTIVIN BETA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          3AFB41BE62ABC0DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
Euteleostel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta A subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length
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                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                    404;
                                                                                                                                                                                                                         223.
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RESULT
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Best Local :
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                        042125
042125;
01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 ... A (FRAUDELLI)
ACTIVIN SUBUNIT A (FRAUDELLI)
AIlurus fulgens (Lesser panda).
                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                      ACTIVIN BETA B (FRAGMENT).

Pagrus major (Red sea bream) (Chrysophrys major).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cioning of the activin gene A subunit mature peptide panda related animals."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   Pfam; PF00019; TGF-beta; 1. ProDom; PD000357; TGF-beta; 1. SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95KP1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Sparidae; Pagrus.
                                                                                            SEQUENCE
                                                                                                                             Glycoprotein.
                                                                                                                                                                                                                                                                     TISSUE-OVERY;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=143350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                       PROSITE; PS00250; TGF_BETA; 1
                                                                                                                                                                                     InterPro; IPR001839; TGF-beta.
                      226 RVEGKHRVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 GIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w
QADNKHRIRKRGLECDGSSSLCCRQQFYIDFRLIGWNDWIIAPSGYFGNYCEGNCPAYMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVINHYRMRGRSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY029555; AAK40342.1;
                                            Similarity
59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
119 AA;
                                                                                          119 AA;
                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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; 13328 MW;
                                                                                                        119
                                                                                            13455 MW;
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51.3%;
                                                        19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                              25;
                                            Score 367.5;
Pred. No. 5e-2
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 368;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                            EFB0E9E9AD1FA888 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fissipedia;
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                                              ع 367.5; الم
                                                                                                                                                                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; DB 6;
. 4.5e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
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                                              32;
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                                              Indels
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                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Wang X., Wang Y., Wang X.;

Wang X., Wang Y., Wang X.;

Wang X., Wang Y., Wang X.;

Wang X., Wang X.;

Wang X., Wang X.;

Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ursus malayanus (Malayan sun bear) (Helarctos malayanus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalla; Eutheria; Carnivora; Fissipedia; Ursidae; Helarctos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACTIVIN SUBUNIT A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95N79
Q95N79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Wang X., Wang Y., Wang X.;
"Cloning and Analysis of Activin Beta-A subunit in Giant Panda.";
"Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ailuropoda melanoleuca (Giant panda).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACTIVIN BETA-A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9634;
297 AVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                            237 GIDCQGGSRMCCRQEFFVDFREIGWNDWIIOPEGYAMNFCTGQCPLHVAGMPGISASFHT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF350256; AAK38654.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 AVLNILKANAAAGTTGRGSCCVPTSRRPLSILYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 GMPGISASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIP 342
                                                                                                                                                                                                                                                                                                                    Loca1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GVPGSASSFHTAVVNQYRMRGMS-PGSMNSCCIPTKLSTMSMLYFDDEYNIVKRDVP 119
                                                                                 GLECDGKVNICCKKOFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHS 62
                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           13309 MW; 914DFB2F25D8218A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.8%; Score 367; DB 6; Length 119; S1.3%; Pred No. 5.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13309 MW; 914DFB2F25D8218A CRC64;
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                                                                                                                                                                                                                                                                                                                                     DB 6; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Ailuropoda.
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            Search completed: October 12,
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                                                                                                                                                                                         Matches
                                                                                                                                                                                                                      Query Match
 time :
                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
ProDom: PD000357; TGF-beta; 1.
SMART: SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TIEMBLIEL 12, Created)
01-NOV-1999 (TIEMBLIEL 12, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation updat
ACTIVIN BETA B PROTEIN (FRAGMENT).
INHBB OR ACTIVIN BETA B.
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                                                                                                  PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR002400; GF_cysknot.
InterPro: IPR002405; Inhibin_alpha
InterPro: IPR001839; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endoderm by FGF.";
Development 126:3067-3077(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SINILARITY: BELONGS TO THE TGF-BETA FAMILY EMBL; AJZ38981; CAB43092.1; -. HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derived TGF-(beta) family signals and discrimination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99307072; PubMed-10375499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W6T9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09W6T9
                                                                                   293 SFHTAVLNLLKANA-AAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                   234 RRRGIDCOGGS-RMCCROEFFVDFREIGWNDWIIOPEGYAMNFCTGOCPLHVAGMPGISA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Induction of the mesendoderm in the zebrafish germ ring by yolk cell-
derived TGF-(beta) family signals and discrimination of mesoderm and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7955;
                                                              75
                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 TVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC 117
                                                      SFHTAVVNQYRMRGMSPGSV--NSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 132
                                                                                                                   RGSGFECDGNNGGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCPAYMAGVPGSAS 74
44 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZDB-GENE-990415-2; inhbb.
                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                      138 AA;
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                TGF-beta;
                                                                                                                                                                           19.3%; Score 357; DB 13; Length 150.8%; Pred. No. 6.9e-28; 24: Mismatches 31; Indels
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                                                                                                                                                                                                                Length 138;
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